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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: August 26, 2002, 10:04:25; Search time 45.87 Seconds

(without alignments)
52.370 Million cell updates/sec
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Title: US-09-701-623C-84
Perfect score: 135
Sequence: 1 CGETYKSTVSHPDLPREVVRSIAKC 25
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters:

283138

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir4:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ig epsilon-chain Ig epsilon chain C
IgE chain C3 regio
IgE chain C3 regio
Ig epsilon chain C
Ig epsilon chain C
Ig upsilon chain C
Ig upsilon chain C
Ig upsilon chain C
Ig v heavy chain (
IepA protein homol
Ig epsilon chain C
Ig P-binding membra
GTP-binding membra
GTP-binding membra
GTP-binding membra
GTP-binding membra
GTP-binding protei
probable GTPase GTP-binding protei
Ig mu chain C regi
hypothetical prote
Ig mu chain C regi
hypothetical prote Ig alpha-2 chain C Ig alpha-2 chain C Ig alpha-2 chain C Ig alpha-2 chain -Ig mu heavy chain Ig mu chain C regi Description SUMMARIES EHHU 168730 168726 EHMS EHMSS 164042 BVECLA C91058 A85903 AE0829 B71561 B81714 S60266 B22360 I56230 MHHUBT S43147 B46529 S70214 I54421 C22360 136948 r19571 338864 F87377 A2HU ü B Query Match Length 599 602 684 684 394 648 Result Š.

A; Molecule type: DNA A; Residues: 1-428 <PLA> A; Residues: 1-428 <PLA> A; Cross-references: GB:L00022; GB:J000227; GB:V00555; NID:g185035 B; Ucda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T. EMBO J. 1, 1539-1544, 1982 A; Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseu A; Reference number: A23195; MUID:84207910

A;Molecule type: DNA A;Residues: 2-428 <UED> A;Cross-references: GB:J00222; NID:g184755

Igepsilon chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999 C;Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999 C;Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; R;Flanagan, J.G.; Rabbitts, T.H. EMBO J. 1, 655-660, 1982 A;Tille: The sequence of a human immunoglobulin epsilon heavy chain constant region (A;Reference number: A22771; MUID:84236029

292 GETYQCRVTHPHLPRALVRSTTK 314

QQ

Ig mu chain C regi	Ig mu chain C regi	Ig mu chain C regi	Ig heavy chain - h	Ig mu chain C regi	GTP-binding protei	probable GTP-bindi	Ig mu chain precur	hypothetical prote	Ig gamma 3 chain c	Ig gamma 1 chain c	GTP-binding protei	G-protein LepA - A	GTP-binding protei	GTP-binding protei
S37768 S03961	MHRB	МННОМ	S15590	MHRBM	D82073	AD0331	S14683	T15183	147161	147158	G83550	H70448	D86763	B95139
7 0	7 –1	Н	~	Н	~	7	~	~	~	N	~	7	7	7
453	458	473	474	479	597	599	627	893	328	328	599	900	607	607
37.8	37.8	37.8	37.8	37.8	37.8	37.8	37.8	37.4	37.0	37.0	37.0	37.0	37.0	37.0
m r														
51 3	51	51	51	51	51	51	51	50.5	20	20	20	20	20	20

ALIGNMENTS

us-09-701-623c-84.open.rpr

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lubrio.

19E chain C3 region - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 0.2-Aug-1996 #text_change 21-Jan-2000
C; Accession: 168730
R; Shinkal, Y: Nakauchi, H: Honjo, T.; Okumura, K.
Imunuogenetics 27, 288-292, 1988
A; Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic aci
A; Reference number: 154443; MUID:88152907
A; Accession: 168730
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-107 CRESA
A; Cross-references: GB: M22933; NID:9194464; PIDN:AAA37915.1; PID:9194469
C; Superfamily: immunoglobulin C region: immunoglobulin homology
F; 22-90/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: 168726
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
          A;Cross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:g263169
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Pred. No. 0.01;
4; Mismatches 6; Indels
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                                                  A; Experimental source: B cell myeloma U-266
A; Note: sequence extracted from NCBI backbone (NCBIP:125299)
A; Accession: A46536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.9%; Score 66; DB 2; ilarity 52.2%; Pred. No. 0.013; Conservative 3; Mismatches
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ilarity 56.5%;
Conservative 4
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Best Local Similarity
Matches 13; Conserv
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Best Local Similarity
Matches 12; Conserv
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R;Zhang, K.; Saxon, A.; Max, E.E.

"Exp. Med. 176, 233-234, 1992

A;Title: Med. unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A;Reference number: PH1214; MUID:92308839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Status: nucleic acid sequence not shown
A Molecule type: mRNA
A 
                                                                                                                                                                                                                                                                                                                                                                                           R;Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sugi
Nucleic Acids Res. 11, 719-726, 1983
A;Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha
A;Reference number: A93491; MUID:83168897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragmen
A;Reference number: S02438; MUID:88083554
A;Accession: S02438
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A;Title: Characterization of four novel epsilon chain mRNA and a comparative analysis
A;Reference number: A46536; MUID:93122085
A;Accession: C46536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A93491
A;Molacule type: mRNA
A;Residues: 1-428 SEEN
A;Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
R;Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A;Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A;Reference number: A90824; MUID:83001945
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 320-428 <22H2>
A;Experimental source: myeloma U266-derived cell line AF-10
A;Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
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A; Residues: 382-426 <HEL>
A; Residues: 382-426 <HEL>
A; Cross-references: GB:S55273; NID:g263166; PIDN:AAB24857.1; PID:g263167
A; Experimental source: B cell myeloma U-266
A; Note:, sequence extracted from NCBI backbone (NCBIP:125297)
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A;Residues:\_382-391 <HE2>
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                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 320-428 <ZHA>
A;Cross-references: EMBL:X63693; GB:S38668; NID:g32987
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Gaps

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Gaps

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A; Molecule type: mRNA
A; Residues: 'N', 169-307,'L',309-342 <KIN>
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52.28;
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Best Local Similarity 52.2%;
Matches 12; Conservative
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Best Local Similarity 52.2
Matches 12; Conservative
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Matches 12; Conservative
        A; Contents: myeloma IR162
A; Accession: A90937
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C; Species: Join-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C; Accession: A02144
R; Liu : Cforning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.
A; Reference number: A02144; MUID:83117774
A; Reference number: A02144; MUID:83117774
A; Residues: 1-388 cLIU>
A; Residues: 1-388 cLIU>
A; Cross-references: GB:J00476; NID:9194875; PIDN:AAA38085.1; PID:9387220
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin c region; immunoglobulin homology
C; Superfamily: immunoglobulin homology (fragment) cIMI>
F; 81-144/Domain: immunoglobulin homology <IMI>
F; 81-44/Domain: immunoglobulin homology <IMI>
F; 81-45/Domain: immunoglobulin homology <IMI>
F; 81-45/Domain immunoglobulin homology <IMI
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Tobec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accession: A93442; A90937; A02143
R;Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A;Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
A;Reference number: A93442; MUID:83064537
A;Reference number: A93442; MUID:83064537
A;Residues: 1-429 <HEL>
A;Residues: 1-429 <HEL>
A;Residues: 1-429 <HEL>
A;Experimental source: strain LOU/c/Wsl, immunocytoma IR2
B;Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
A;Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, A;Reference number: A90937; MUID:83182019
Immunogenétics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid
A;Reference number: 154443; MUID:88152907
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                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-107 <RES>
A;Cross-references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460
C;Superfamily: Immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                      A;Accession: 168726
A;Status: preliminary; translated from GB/EMBL/DDBJ
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F;290-361/Domain: immunoglobulin homology <IM4>
F;10,51,62,133,205,228,332,382/Binding site: car
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83 GYGYQCIVDHPDFPKPIVRSITK 105
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Matches 12; Conservative
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Cycomplex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into cysuperfamily: immunoglobulin c region; immunoglobulin homology cysuperfamily: immunoglobulin c region; immunoglobulin homology cysuperfamily: immunoglobulin homology cimes: immunoglobulin homology cim
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C;Species: Anas platyrhynchos (domestic duck)
C;Species: Anas platyrhynchos (domestic duck)
C;Bate: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
C;Accession: S43147
R;Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
Submitted to the EMBL Data Library, March 1994
A;Description: Evidence from duck immunoglobulin genes that IgY is the common A;Reference number: S43145
A;Accession: S43147
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;353-421/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
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0.058;
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Pred. No. 0.076;
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Pred. No. 0.11;
3; Mismatches
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Pred. No.
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A.Gene: lepa
C, Superfamily: GTP-binding membrane protein lepa; translation elongation factor Tu ho
C, Superfamily: GTP-binding membrane protein; nucleotide binding; P-loop
C, Superfamily: translation elongation factor Tu homology <ETU>
F;1-134/Domain: translation elongation factor Tu homology <ETU>
F;11-18/Region: nucleotide-binding motif A (P-loop)
F;131-134/Region: GTP-binding NKXD motif
F;162-164/Region: GTP-binding SAK/L motif
F;17,18,53,131,132,134,162/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #
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C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
c; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
c; Complex: An immunoglobulin cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin c region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 15-183 / Domain: immunoglobulin homology < IMM2>
F; 220-286 / Domain: immunoglobulin homology < IMM3>
F; 320-286 / Domain: immunoglobulin homology < IMM3>
F; 325-36 / Domain: immunoglobulin homology < IMM3>
F; 3275, 122-181, 1227-286, 332-394 / Disulfide bonds: #status predicted
F; 43, 84, 167, 239, 262, 417/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Haman, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
C;Scayer, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
A;Authors: Genbm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Title: Whole-genome random sequenching and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630
                                              C;Accession: A02145
R;Ishida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.
EMBO J. 1, 1117-1123, 1982
A;Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison A;Reference number: A90966; MUID:84236092
A;Accession: A02145
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A; Residues: 1-423 <ISH>
A; Note: the sequence was determined from the germline gene C; Genetics:
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                                                                                                                                                                                                                                                                               N.Alternate names: Ig gamma chain (7.85)
C;Species: Anas platyrhynchos (domestic duck)
C;Species: Anas platyrhynchos (domestic duck)
C;Accession: B46529; S20759
R;Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
A;Title: Structural relationship between the two IgY of the duck, Anas platyrhynchos: mc
A;Reference number: A46529; WUID:93017865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Photobacterium sp. (ildyment)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 02-Feb-2001
C;Accession: S70214
R;Chi, E.; Bartlett, D.H.
MAL Microbiol. 17, 713-726, 1995
A;Title: An rpoE-like locus controls outer membrane protein synthesis and growth at cold A;Reference number: S70210; MUID:96111491
A;Accession: S70214
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A. Residues: 1-137 < CHI>
A. COSS - references: EMBL:L41667; NID:g777746; PIDN:AAB31927.1; PID:g777751
A. Cross - references: EMBL:L41667; NID:g777746; PIDN:AAB31927.1; PID:g777751
A. Cross - references: EMBL:L41667; NID:g777746; PIDN:AAB31927.1; PID:g777751
C. Superfamily: GTP-binding membrane protein lepA; translation elongation factor Tu homol C; Reywords: GTP binding nucleotide binding: P-loop
F:5-134/Pommain: translation elongation factor Tu homology < FTU>
F:11-18/Region: uncleotide-binding motif A (P-loop)
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A; Note: sequence extracted from NCBI backbone (NCBIP:116127)
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 37-120/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57; DB 2; Length 572;
Pred. No. 1.8;
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Pred. No. 1.1;
2; Mismatches
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ilarity 52.2%;
Conservative
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Best Local Similarity 46.4%;
Matches 13; Conservative
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Best Local Similarity
Matches 12; Conserv
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A; Molecule type: mRNA
A; Residues: 1-572 <MAG>
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EHMSS
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Search completed: August 26, 2002, 10:04:26
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Best Local Similarity
Thes 13; Conserve
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A;Molecule type: DNA
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BVECLA .

GTP-binding membrane protein lepA - Escherichia coli
C;Species: Escherichia coli
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C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;C;Date: 31-Mar. 1988 4seguence_revision 05-Dec-1997 #text_change 19-Jan-2001
C;Accession: H65034, A2627
A;Blattner, F. R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
A; Reset D.J.; Mau. B.; Shao, Y.
A; Perna and A; Species and A; Species and A; Stetus: And A; Species and A; Stetus: And A; Species and 
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Superfamily: GTP-binding membrane protein lepA; translation elongation factor Tu homol
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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Matches 13; Conservative
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A; Residues: 1-599 <HAY>
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RESULT 15
A85903
GTP-binding membrane protein lepA - Escherichia coli (strain O157:H7, substrain EDL93
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C;Accession: A85903
                                                                                                                                                                                                                                                                                                                                                    R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
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A;Experimental source: strain O157:H7, substrain EDL933
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illarity 46.4%; Pred. No. 5.2;
Conservative 2; Mismatches
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2 GETYK----STVSHPDLPREVVRSIAKC 25
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[2]
SEQUENCE FROM N.A.
MEDILINE=83001945; PubMed=6288268;
MAX E.E., Battey J., Ney R., Kirsch I.R., Leder P.;
"Duplication and deletion in the human immunoglobulin epsilon genes.";
Cell 29:691-699(1982).
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PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).
Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
(In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.1-36, Marcel Dekker, New York (1978).
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SEQUENCE FROM N.A.
MEDLINE-84236029; PubMed-6234164;
MEDLINE-84236029; PubMed-6234164;
Flanagan J.G., Rabbitts T.H.;
"The sequence of a human immunoglobulin epsilon heavy chain constant region gene, and evidence for three non-allelic genes.";
EMBO J. 1:655-660(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-81186897; PubMed-6300763;
MEDLINE-8186897; PubMed-6300763;
Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,
Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
"Molecular cloning and nucleotide sequencing of human immunoglobulin
epsilon chain cDNA.";
Nucleic Acids Res. 11:719-726(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-84207910; PubMed-6327276;
MEDLINE-84207910; Nushida Y., Hisajima H., Honjo T.;
"Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudogene that lacks introns.";
EMBO J. 1:1539-1544(1982).
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SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.
MEDLINE-83065234; Pubmed-6815656;
MEDLINE-83065234; Pubmed-8015656; Derby
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(Rel. 01, Last sequence update)
(Rel. 40, Last annotation update)
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Copyright (c) 1993 - 2000 Compugen Ltd.
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    protein search, using sw model

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LEPA_CHLPN
ASPH_BOVIN
YEO6_YEAST
BAR1_MOUSE
BAR1_RAT
DN71_SULSO
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DN72_SULSH
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                          SEQUENCE OF 34-421 FROM N.A. MEDLINES 8311774; Pubmed-6818553; Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.; "Cloning and nucleotide sequence of mouse immunoglobulin epsilon
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                                                                              Submitted (APR-1986) to the EMBL/GenBank/DDBJ databases
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comparison with the human epsilon gene sequence."; \rm EMBO~J.~1:1117-1123(1982).
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
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EMBL; X01857; CAA25978.1; --
FTR; A00145; EHMSS.
PTR; A00144; EHMS.
HSSP; P01854; 11GE.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_C1.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003607; Ig_C1.
SMART; SM00410; Ig_11ke; Z.
SMART; SM00407; IG; Z.
PROSITE; PS00290; IG_MHC; 3.
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SEĞÜENCE FROM N.A.
MEDLINE-84236092; Pubmed-6329728;
Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
"The nucleotide sequence of the mouse immunoglobulin epsilon gene:
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N-L (IN REF. 2, POSSIBLY DUE TO POLYMORPHISM).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Pred. No. 0.0027;
Wismatches 6; Indels
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25C4CA072AA558A0 CRC64;
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                    Padian E.A., Davies D.R.; "A model of the F-C- of immunoglobulin E."; Submitted (JUL-1993) to the PDB data bank.
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InterPro; IPR003597; Ig_c1.
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56.5%;
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SMART; SM00407; IGc1; 4.
PROSITE; PS00290; IG_MHC; 3.
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Best Local Similarity 56.55
Matches 13; Conservative
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PIR; A22771; A22771.
PIR; A23195; A23195.
PDB; 11GE; 15-UUL-92.
MIM; 147180;
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16-OCT-2001
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                 Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.; "Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 205-306 FROM N.A.
MEDLINE=82174576; PubMed=6803238;
Hellman L., Pettersson U., Bennich H.;
Characterization and molecular cloning of the mRNA for the heavy (epsilon) chain of rat immunoglobulin E.";
Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
                                                                                                                                                                                                                                                                                              SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
MEDLINE-83182019; PubMed=6820340;
Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
Ka cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
construction, identification, and DNA sequence.";
DNA 1:335-343(1982).
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.9%; Score 66; DB 1; Length 429, 52.2%; Pred. No. 0.015;
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-> L (IN REF. 2).
D2970B34EF8A72B0 CRC64;
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Immunoglobulin domain; Immunoglobulin C region.
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
LEPA OR HI0016
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                                                                                                              SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
                                                                                                                                                                                                                                                     Nucleic Acids Res. 10:6041-6049(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J00744; AAA41379.1; ALT_INIT
                                                                                                                                                         MEDLINE-83064537; PubMed=6292865;
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InterPro; PRR003006; Ig_MHC.
InterPro; IPR003009; Ig_C1.
InterPro; IPR003609; Ig_like.
SMART; SM00410; Ig, 4.
SMART; SM00410; IG_like; 3.
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308 P
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Best Local Similarity 52.2
Matches 12; Conservative
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429 AA;
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                                                                     NCBI_TaxID=10116;
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DE GTP-DCT
GN LEPA 00
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       MEDLINE=95350630; PubMed=7542800; MEDLINE=95350630; PubMed=7542800; Pelsischmann R.D., Adams M.D., Mhite O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Pritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                  Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: PRESENT IN THE CYTOPLASMIC MEMBRANE AND IS
-!- SUBCELLULAR LOCATION: PRESENT IN THE CYTOPLASMIC MEMBRANE AND IS
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                     "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 598
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GTP (BY SIMILARITY).
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Pred. No. 1.5;
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Pfam; PF03144; GTP_EFTU_D2; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
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66333 MW;
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Best Local Similarity 46.49
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598 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                             influenzae Rd.
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                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                      Gaps
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(200i).
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
LEPA SUBFAMILY.
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SEQUENCE FROM N.A.
MEDILINE-97426617; Pubmed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Kiley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Maŭ B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A. MEDIANE-85207751; PubMed-2987248; March P.E., Inouye M.; Characterization of the lep operon of Escherichia coll. Identification of the promoter and the gene upstream of the signal peptidase I gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                               Score 54; DB 1; Length 598;
Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                     9; Indels
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                                                                                                                                                                                                                                                                                                                     2; Mismatches
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                                                                                                                                  EMBL, AE006042; AAK02147.1; -.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
Pfam; PF00109; GTP_EFTU, 1.
Pfam; PF03144; GTP_EFTU_D2; IPR0715; PR007315; ELONAATNECT.
PROSITE; PS00301; EFACTOR_GTP.
GTP_binding; Complete_proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 260:7206-7213(1985)
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LEPA OR B2569 OR 23851 OR ECS3435.
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598 AA; 66211 MW;
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46.4%;
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Best Local Similarity 46.43
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=015:H7 / RIND 0509952;
MEDLINB=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnshi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
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TDAVRCSARTGVGVQDVLERLVRDIPPPEG -> HRRGALF
SENRRWCAGRSRTSGARHSAAGS (IN REF. 1 AND
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SEQUENCE FROM N.A.
STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
MEDLINE-21074935; PubMed-11206551;
MEDLINE-21074935; PubMed-111, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Rotheck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
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91E3678557A46D49 CRC64;
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HSSP; P1351; 1DAR.

EcoGene; EG10529; lepA.

InterPro; IPR000195; GTP_EFTU.

InterPro; IPR000195; GTP_EFTU.

Pfam; PF00009; GTP_EFTU.D2.

Pfam; PF00144; GTP_EFTU.D2.

PROSITE: PS00301; EFETU.D2: 1.

PROSITE: PS00301; EFETU.D2: 1.

NP_BIND 11 18 GTP (BY SIMILAN NP_BIND 131 134 GTP (BY SIMILAN NP_BIND NP_BI
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EMBL, AE005487; AAG57685.1; -
EMBL, AP002562; BAB36858.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latraille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: PRESENT IN THE CYTOPLASMIC MEMBRANE AND IS ALSO FOUND IN THE PERIPLASM.
                                                                                       Gaps
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LEPA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                       01-NOV-1991 (Rel. 20, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2003 (Rel. 41, Last annotation update)
01-MAR-2003 (Rel. 41, Last annotation update)
03-Morella typhimurium, and
03-Monotalla typhimurium, and
03-Morella typhimuriu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  van Dijl J.M., van den Bergh R., Reversma T., Smith H., Bron S.,
                                                                                       4 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609;
                                       Length 599
                                                                                9; Indels
                                       ; DB 1;
                                    Score 54; DB 1; Pred. No. 1.5; 2; Mismatches
                                                                                                                            2 GETYK----STVSHPDLPREVVRSIAKC 25
                                                                                                                                                                      68 GETYQLNFIDTPGHVDFSYEVSRSLAAC 95
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MEDLINE-91066835; PubMed-2250650;
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Mol. Gen. Genet. 223:233-240(1990).
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MEDLINE=21534947; PubMed=11677608;
                                       40.08;
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                                                            Best_Local Similarity 46.4
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                     STANDARD;
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P23698;
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                                         Query Match
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LEPA_SALTY
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
LEPA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                               Length 599
                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
EMBL; AE008817; AALLIT.;

EMBL; X54933; CAA38695.1; -.

R EMBL; AL627275; CAD02785.1; -.

R PIR; S12019; S12019.

DR InterPro; IPR000795; GTP_EFTU.

DR Membrane; GTP-binding; Complete proteome.

W Membrane; GTP-binding; Complete proteome.

I 18 GTP (BY SIMILARITY).

R SIMILARITY).

""" 'RY SIMILARITY).
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DOBD7FBE947157DA CRC64;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 1;
Pred. No. 1.5;
2; Mismatches
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(Rel. 40, Last annotation update)
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InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR003575; Small_GTPase.
Pfan; PF00109; GTP_EFTU_1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATHET.
PROSITE; PS00301; EFACTOR_GTP; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 GETYQLNFIDTPGHVDFSYEVSRSLAAC 95
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MEDLINE-20150255; Pubmed-10684935;
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NP_BIND 16 23 GT
NP_BIND 81 85 GT
NP_BIND 135 138 GT
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                                                                                                                                                                                                                                                                                                  599 AA; 66538 MW;
                                                                                                                                                                                                                                                                                                                                                                          ch 40.0%;
1 Similarity 46.4%;
13; Conservative 2
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Best Local Similarity
Matches 13; Conserv
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LEPA OR TC0334
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16-OCT-2001
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NP_BIND
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SEQUENCE (MYELOMA PROTEIN LAN)
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                                 Ig MU chain C region.
Canis familiaris (Dog
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Matches 12; Conserv
                                                                              NCBI_TaxID=9615;
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ID ALC2_HUMAN
AC P01877;
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                                                                                                                                                                                                                                                                                                MEDLINE-99000809; PubMed-9784136; Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                       Chlamydia trachomatis.";
Science 287:754-759(1998).
-1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
LEPA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                             "Genome sequence of an obligate intracellular pathogen of humans:
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                                Length 602;
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                                                       Indels
67378 MW; 1EEA355FF60EBF3D CRC64;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
98F67C990196EEC4 CRC64;
                                                                                                                                                                                                                                 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                               Score 54; DB 1;
Pred. No. 1.5;
                                                                                                                                                                            (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                       602 AA
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                                                     2; Mismatches
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InterPro; IPR004161; GTP_EFTU_D2.
Pfam; PF00009; GTP_EFTU_I.
PRIMIPS: PR003144; GTP_EFTU_D2; 1.
PRIMIPS: PR00315; ELOMGATHRCT.
PROSITE; PS00301; EFACTOR_GTP; FALSE_NEG.
GTP-binding; Complete proteome.
                                                                           2 GETYK----STVSHPDLPREVVRSIAKC 25
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602 AA; 67435 MW;
                              ch 40.0%;
1 Similarity 46.4%;
13; Conservative
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602 AA;
                                            Best Local Similarity
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SEQUENCE FROM N.A.
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084067;
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P01874; →
SEQUENCE
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SEQUENCE
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LEPA_CHLTR
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SEQUENCE FROM N.A.
MEDLINE=84130179; PubMed=6421489;
Flanagan J.G., Lefranc M.-P., Rabbitts T.H.;
"Mechanisms of divergence and convergence of the human immunoglobulin alpha 1 and alpha 2 constant region gene sequences.";
cell 36:681-688(1984).
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Masserman R.L., Capra J.D.;
Masserman R.L., Capra J.D.;
Masserman R.L., Capra J.D.;
Masserman R.L., Capra J.D.;
Minterspecies homology for the IgM class.";
Anterspecies homology for the IgM class.";
PIR; A02169; MHDG.
HSSP; P01857; IFC1.
InterPro; IPR0033006; Ig_MHC.
InterPro; IPR0033597; Ig_c1.
InterPro; IPR003600; Ig_like.
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MEDLINE=78137069; PubMed=416441;
Torano A., Putnam F.W.;
"Complete amino acid sequence of the alpha 2 heavy chain of a human 19A2 immunoglobulin of the A2m (2) allotype.";
Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                McCumber L.J., Capra J.D.; "The complete amino-acid sequence of a canine mu chain."; Mol. Immunol. 16:565-570(1979).
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50.0%; Pred. No. 1.9;
Live 2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin domain; Immunoglobulin C region.
NON_TER 1 1 SEGUENCE 450 AA; 48895 MW; 9D460DA9D1012F5D
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                      SEQUENCE OF 1-177 (MOO) MEDLINE-80077682; PubMed-117299;
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Mammalia; Eutheria; Primates;
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SMART; SM00410; IG_like; 2.
SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 3.
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Mismatches

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Conservative
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Best Local Similarity
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                                                                                                                                                                                                 NCBI_TaxID=9606
                                                                                                                                                                                                                                                     Hilschmann N.;
                                                                                                                      20-MAR-1987
                                                                                                                               20-MAR-1987
16-OCT-2001
                                                                                                  MUCB_HUMAN
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P01871;
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MUC_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE)
                                                                                                                 SECRETION: IG ALPHA IS THE MAJOR IMMUNOGLOBULIN CLASS IN BODY SECRETIONS. IT MAY SERVE BOTH TO DEFEND AGAINST LOCAL INFECTION AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL IMMUNOLOGIC SYSTEM.
                                                                                                                                                              -!- SUBUNIT: MONOMERIC OR POLYMERIC.
-!- MISCELLANEOUS: THE SEQUENCE OF THE A2M(1) ALLOTYPE IS SHOWN.
           Suzukida Y., Wang C.-C., Putnam F.W.;
Structure of the A2m(1) allotype of human IgA -- a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin domain; Immunoglobulin C region; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERCHAIN (WITH LIGHT CHAIN)
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/FTIG=VAR_003879.

P -> R (IN A2M(2) ALLOTYPE).

/FTIG=VAR_003880.

F -> Y (IN A2M(2) ALLOTYPE).
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N-LINKED (GLCNAC. . .).
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N-LINKED (GLCNAC. .).
P -> S (IN A2M(2) ALLOT
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                                          Proc. Natl. Acad. Sci. U.S.A. 76:1104-1108(1979)
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                                                                                                "The structure and function of human IgA."; Biochem. J. 271:285-296(1990).
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                                                                          MEDLINE=91054387; PubMed=2241915;
MEDLINE-79180140; PubMed-286295;
                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 2.
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PIR; B22360; B22360.
C22360; C22360.
HSSP; P01810; ZFBJ.
MIM; 147000;
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Score :

37.8%; 39.1%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Barnikol-Watanabe S., Mihaesco E., Mihaesco C., Barnikol H.U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                          "The primary structure of mu-chain-disease protein BOT. P
amino-acid sequence of the N-terminal 42 postitions.";
Hoppe-Seyler's Z. Physiol. Chem. 365:105-11811984).
-!- MISCELLANEOUS: THIS PROTEIN HAS NO V REGION HOMOLOGY
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Pred. No. 2.7;
                                                                                                                                                                                             20-MAR-1987 (Rel. 04, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 MU heavy chain disease protein (BOT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 17, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                         391 AA
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                      236 GERFTCTVTHTDLPSPLKQTISR 258
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2 GETYKSTVSHPDLPREVVRSIAK 24
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01-FEB-1991 (Rel. 17, Last sequ
01-MAR-2002 (Rel. 41, Last anno
                                                                                                                                                                                (Rel. 04, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43057 MW;
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HSSP; P13760; 2SEB.
INTERPRO; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
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39.1%;
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IGHM.
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156
262
391 AA;
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EMBL; X13920; CAA32113.1; ALT_INIT
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CH2.
CH3.
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HSSP, P01857; 1FC1.
InterPro; IPR030066; 1g_MHC.
InterPro; IPR003597; 1g_C1.
InterPro; IPR003609; 1g_like.
Pfam; PF00047; 1g; 4
                                                                                                                                                                                                     MW;
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Best Local Similarity 39.1%;
Matches 9; Conservative
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P20768;
DISULFID
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                                             MEDLINE-75059123; Pubmed-4803843; Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.; Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.; The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mutype), subgroup H III. Architecture of the complete IgM-molecule."; Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 299-387 AND 438-454 FROM N.A. MEDLINE-81077306; PubMed-6777778; Dolby T.W., Devuono J., Croce C.M.; Dolby T.W., Devuono J., Croce C.M.; Cloning and partial nucleotide sequence of human immunoglobulin muchain cDNA from B cells and mouse-human hybridomas."; Proc. Natl. Acad. Sci. U.S.A. 77:6021-6031(1980).
-!- MISCELLANEOUS: ALL 4 COMBINATIONS OF THE S/G & V/G POLYMORPHISMS AT POSITIONS 192 AND 216 HAVE BEEN OBSERVED IN HUMAN MU CHAINS.
                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE FROM N.A. MEDIINE-82059479; PubMed-6795593; Rabbitts T.H., Forster A., Milstein C.P.; "Human immunoglobulin heavy chain genes: evolutionary comparisons of C mu. C delta and C gamma genes and associated switch sequences."; Nucleic Acids Res. 9:4509-4524(1981).
                                                                                                                                                                                                                                      SEQUENCE (WALDENSTROM'S OU), DISULFIDE BONDS, AND CARBOHYDRATES.
MEDLINE-74005511; PubMed-4742735;
Putnam F.W., Florent G., Paul C., Shinoda T., Shimizu A.;
Complete amino acid sequence of the Mu heavy chain of a human IgM immunoglobulin.";
Science 182:287-291(1973).
                                                                                                                                                                                        "The primary structure of the constant part of mu-chain-disease protein \mathtt{BOT}.."\,;
                                                                                                                                       REVISIONS TO GAL.
MEDLINE-81066716; Pubmed-6777162;
Milaesco E., Barnikol-Watanabe S., Barnikol H.U., Mihaesco C.,
Hilschmann N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
NON_TER
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                                      SEQUENCE (WALDENSTROM'S MACROGLOBULIN GAL).
             Nucleic Acids Res. 18:4278-4278(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, X17115; CAA34971.1; ALT_SEQ. EMBL, X57086; -; NOT_ANNOTATED_CDS. PIR, A02162; MHU.
HSSP, P13760; 2SEB.
MIM; 147020; -
GlycoSulteDB, P01871; -,
InterPro; IPR003507; Ig_Gl.
InterPro; IPR003507; Ig_Gl.
InterPro; IPR003507; Ig_l.
InterPro; IPR003507; Ig_l.
SMART; SM00410; IG_like; I.
SMART; SM00407; IG_Like; I.
                                                                                                                                                                                                                 Eur. J. Biochem. 111:275-286(1980).
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INTERCHAIN (WITH A HEAVY CHAIN IN ANOTHER OF THE 5 TETRAMERIC SUBUNITS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Insectivora; Soricidae; Suncus.
                                                                                                                           INTERCHAIN (WITH A HEAVY CHAIN).
N-LINKED (GLCNAC. .).
YETIG—CAR_000219.
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SMART; SMO0407; IGC1; 3.
PROSITE; PSO0290; IG_MC; 3.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51; DB 1; Length 454;
Pred. No. 3.2;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR_003904.
21EC72EADC56922E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR_003903
V -> G.
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no wat modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                               INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).

BY SIMILARITY.
INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
BY SIMILARITY.
                                                                                                                                                                                                                                                             Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia: Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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Pred. No. 3.2;
6; Mismatches 8; Indels
                                                                                                                                                                             LINKED (GLCNAC. . .) (POS 56C8C086DA4462E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG MU Chain C region.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 4.
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Best Local Similarity 39.1%;
Matches 9; Conservative
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P03988;
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                                                        INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).
                      INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE)
BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 3.2;
5; Mismatches 8; Indels
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Matches 10; Conserv
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CARBOHYD
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Search completed: August 26, 2002, 10:17:04 Job time: 700 sec

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002099 caenorhabdi
0920420 listeria mo
091598 pseudomonas
0974k5 streptococc
092bn4 listeria in
0992v8 streptococc
091205 mus musculu
048786 arabidopsis
0960c2 drosophila
090444 drosophila
090818 masculu
09682 mus musculu
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09623 mus musculu
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Q30827 ovis aries
Q31270 rattus norv
Q94qa5 rattus norv
Q97ps4 streptococc
Q17621 caenorhabdi
Q91wH4 oryza sativ
Q95tr4 staphylococ
Q2594 plasmodium
Q958y8 rhizobium s
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P79954 xenopus lae
Q981e5 rhizobium l
   sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Photobacterium profundum (Photobacterium sp. (strain SS9)). Bacteria: proteobacteria; gamma subdivision; Vibrionaceae; Photobacterium.

WCBI_TaxID=74109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=SS9;
Chi E., Bartlett D.H.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
U-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RPOE, LEPA AND ORF 2, 3, 4 GENES (FRAGMENT).
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Pred. No. 1.6;
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09NE67
002099
09EV20
0915G8
0915G8
0992V8
0992BW4
0996DE2
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090BE2
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Q9LWH4
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Q25994
Q9R8Y8
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Best Local Similarity 46.43
Matches 13; Conservative
 [1]
SEQUENCE FROM N.A.
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                                       Q57464
Q57464;
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Q57464
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Q9kpb0 vibrio chol
Q96ey0 homo sapien
Q96ga6 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9bszl homo sapien
O9npp6 homo sapien
O99k47 mus musculu
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017620 caenorhabdi
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Q31260 rattus norv
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Q9cm48 pasteurella
                                                                                                                     August 26, 2002, 10:16:21; Search time 66.82 Seconds (without alignments) 64.724 Million cell updates/sec
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Q9bul0 homo sapien
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    562222 seqs, 172994929 residues
                                                                                                                                                                                                                      135
1 CGETYKSTVSHPDLPREVVRSIAKC 25
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Listing first 45 summaries
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Q90544
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Q31260
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Q9CM48
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Q96GA6
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_bacteriap:*
sp_archeap:*
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sp_phage:*
sp_plant:*
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16
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Match Length
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SEQUENCE FROM N.A.

STRAIN-ATCC 19089 / CB15;

MEDLINE-21173698; PubMed-11259647;

MEDLINE-21173698; PubMed-11259647;

MEDLINE-21173698; PubMed-11259647;

MAIST Naison W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

R. Naison W.C., Newton A., Stephens C., Phadke N.D., Bly B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

MILEPDACK T., Tran K., Wolf A., Vanathevan J., Ermolaeva M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

"I. SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

REMBL: ABEO05781; JELO.
                                                                                                                                                                             Gaps
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Caulobacter.
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                                                                             D4424A972AE24451 CRC64;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RAT MHC CLASS II RT1 B-BETA2 (FRAGMENT).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.5%; Score 52; DB 16;
46.4%; Pred. No. 17;
tive 1; Mismatches 10;
                                                                                                                                   Score 52; DB 5;
Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                   648 AA
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InterPro; IPR001806; Ras_trnsfrmng
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PRINTS; PRO0449; RASTRINSFRANG.
COMPLETE; PS00301; EFACTOR_GTP; 1.
COMPLETE PROTECOME; GTP-binding.
SEQUENCE 648 AA; 71538 MW; 3E6
                                                                             44297 MW;
Science 282:2012-2018(1998).
EMBL; Z92877; CABO7326.1; -
Interpro; IPR004119; DUF227.
Pfam; PF02958; DUF227; 1.
SEQUENCE 394 AA; 44297 MW;
                                                                                                                                     38.5%;
52.9%;
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                                                                                                                                                                                                                                       Query Match 38.5
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             GTP-BINDING PROTEIN LEPA.
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=69394;
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01-DEC-2001
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Q9A9F4;
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Q31260;
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A Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
Flajnik M.F.; Avila D., Hughes M., Hughes A., McKinney E.C.,
T. A new antigen receptor gene family that undergoes rearrangement and
extensive sometic diversification in sharks.";
Nature 374:168-173(1995).
REMBL; U18701; AAB48195.1; -.
REMBL; U18701; AAB48195.1; -.
RICAPPO; IPR003500; Ig_like.
RICAPPO; IPR003500; Ig_MHC.
RICAPPO; IPR003006; Ig_MHC.
REMART; SM00407; IGcl; 4.
REMART; SM00410; IG_like; 2.
REMART; SM00410; IG_like; 2.
REMART; SM00410; IG_MHC; UNKNOWN_3.
REGEPTOR: RECEPTOR: IG_MHC.
REMART; REGEPTOR: IG_MHC.
REMART; SM00410; IG_Like; 2.
REMART; SM00410; IG_Like; 2.
REMART; SM00410; IG_Like; 2.
REMART; SM00410; IG_Like; 3.
REMART; SM00410; IG_Like; 3.
REMART; SM00410; IG_Like; 4.
REMART; RECEPTOR: IG_MHC; UNKNOWN_3.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                             Ginglymostoma cirratum (Nurse shark).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
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investigating biology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McMurray A.A.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
NOVEL ANTIGEN RECEPTOR.
2FF9D2071CDA6DFD CRC64;
                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NOVEL ANTIGEN RECEPTOR PRECURSOR.
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Last annotation update)
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                                                                                                                   684 AA
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   Created)
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SEQUENCE FROM N.A.
TISSUE-SPLEEN;
MEDLINE-95183140; PubMed-7877689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MED&INE-99069613; PubMed-9851916;
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75224 MW;
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                                                                                                                   PRELIMINARY;
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Best Local Similarity
Matches 10; Conserv
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SEQUENCE FROM N.A.
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STRAIN-PM70;
MEDLINE-21145866; PubMed=11248100;
MAD B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006138; AAK03079.1; -..
HSSP; P00935; 1CS1.
InterPro; IPR000277; Cys_Met_Meta_PP.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                            Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004476; AAH04476.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
SEQUENCE 369 AA; 40565 MW; EB8654C9FB69C5F0 CRC64;
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SEQUENCE 375 AA; 41314 MW; B1A0A0998F473619 CRC64;
                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 41.3 KDA PROTEIN.
HOMO sapiens (Human).
                                                                                                                                                                   369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01053; Cys_Met_Meta_PP; 1.
PROSITE; PS00868; CYS_MET_METAB_PP; 1.
                                                                                                                                                                                                                        Created)
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SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 TYKSTVSHPDLPRE--VVRSIAKC 25
     HSSP; P01857; IFC1.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity
Matches 9; Conserv
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Q9CM48;
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                                                                                                                                                                           Scholler J., Lernmark A.;
Scholler J., Lernmark A.;
"Isolation of a rat immune response gene identical to an alleged mouse a class II beta-chain pseudogene.";
Immunogenetics 22:601-608(1985).
EMBL: M15561; AAA68203.1;
HSSP; P01903; 1A6A.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Eukažyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 2.9;
1; Mismatches 7; Indels
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36450 MW; 7C3D17465CA608CC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FIBRINGGEN A-ALPHA-CHAIN (FRAGWENT).
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SMART; SM00407; ig; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
NON_TER 1 1 1
NON_TER 93 93
SEQUENCE 93 AA; 10605 MW. 300007
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EMBL; D43759; BAA07816.1; -.
HSSP; P02671; 1FZA.
                                                                                                                               STRAIN-WISTAR; TISSUE-KIDNEY; MEDLINE-86084127; PubMed-3865893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93269219; PubMed=8497848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.8%;
52.9%;
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Best Local Similarity 52.3
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341 AA;
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ses 10; Conserv
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                                                       VCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       species.
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Q08284;
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Matches
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Gaps

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Length 375;
 Score 51; DB 4;
37.8%;
 Query Match
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1 CGETYKSTVSHPDLPREVVRSI 22

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Gaps

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09BUIO.
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 65.3 KDA PROTEIN.
HYPOTHETICAL 65.3 KDA PROTEIN.
HYPOTHETICAL 65.4 KDA PROTEIN.
EUKATYOTA: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                           Score 51; DB 11; Length 557;
Pred. No. 20;
1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC006180; AAH06180.1; -. EMBL; BC001872; AAH01872.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 HSSP; P02671; 1FZA.
MGD; MGI:1316726; Fga.
SEQUENCE 557 AA; 61325 MW; C47F496D1BA432DE CRC64;
                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.8%; Score 51; DB 4; 39.1%; Pred. No. 22;
                                                                                                                                                                                                                                                   597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     597 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || : ||:| ||| : ::|::
| 442 GERFICTVTHTDLPSPLKQTISR 464
                                                                                                                                                          2 GETYKSTVSHPDLPREVVRSIAK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR003599; 19.
Interpro; IPR003597; 19_c1.
Interpro; IPR003600; 19_like.
Interpro; IPR003006; 19_MfC.
Interpro; IPR003596; 19_v.
Pfam; PF00047; 19; 5.
SMART; SM00407; 1Gc1; 4.
SMART; SM00407; 1Gc1; 4.
SMART; SM00410; 1Gc1; 1.
                                                                                                                                          1 CGETYKSTVSHPDLPREVVRSI 22
                                                                           Ouery Match 37.8%;
Best Local Similarity 45.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 39.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-RHABDOMYOSARCOMA;
                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BU10
                                                                                                                                                                                                                                                   09BQB8
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                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K., Lehrach H., Poustka A., Lundeberg J.;

The Buropean IMAGE consortium for integrated Molecular analysis of human gene transcripts.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL389978; CAB97534.1;

InterPro; IPR003600; Ig_like.

InterPro; IPR003600; Ig_MHC.

InterPro; IPR003506; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.8%; Score 51; DB 4; Length 416; Best Local Similarity 39.1%; Pred. No. 15; Mismatches 9; Indels Matches 9; Indels
                 7; Indels
                                                                                                                                                                                                                                                                                                                                          Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005467; AAH05467.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416 AA; 44786 MW; 8C41708BBBAB4687 CRC64;
                                                                                                                                                                                   01-0c1-2000 (TrEMBLrel. 15, Created)
01-0C1-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNGGLOBULIN HEAVY CHAIN VARIANT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FIBRINGEN A ALPHA POLYPEPTIDE.
                                                                                                                                                         416 AA.
 Pred. No. 13;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ffan; PF60047; 19; 4.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_11ke; 3.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
1 1 1
SEQUENCE 416 AA; 44786 MW; 8C417
                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                           220 GERFTCTVTHTDLPSPLKOTISR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 GETFTCTAAHPELKTPLTANITK 284
                                              2 GETYKSTVSHPDLPREVVRSIAK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GETYKSTVSHPDLPREVVRSIAK 24
 39.18;
                9; Conservative
                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
Best Local Similarity
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                         09NPP6;
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                 Matches
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Q9NPP6
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SEQUENCE FROM N.A.
STRAINEL TOR NIG961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E. R., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Nature 406:477-483(2000).
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY EMBL; AE004316; AAF95605.1; -. HSSP; P13551; 1DAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLRel. 19, Last an
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                                                                         "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.8%; Score 51; DB 16; Length 597; 42.9%; Pred. No. 22; tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.8%; Score 51; DB 4; Length 613; 39.1%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; ARH11857.1; -.
SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        754ClEE2E3DF0DDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_I
PROSITE; PS00301; EFACTOR_GTP; 1.
Complete proteome; GTP-binding.
SEQUENCE 597 AA, 66029 MW; 754CIEE2E3DF0DDE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          613 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro: IPR002106; AA_tRNA_ligase_II.
Interpro: IPR000795; GTP_EFTU.
Interpro: IPR001806; Ras_trnsfrmng.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: August 26, 2002, 10:16:22 Job time: 713 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GETYK----STVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 GQTYQLNFIDTPGHVDFAXEVSRSLAAC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=PRIMARY B-CELLS FROM TONSILS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || : ||:| ||| : ::|::
GERFTCTVTHTDLPSPLKQTISR 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GETYKSTVSHPDLPREVVRSIAK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00315; ELONGATNFCT. PRINTS; PR00449; RASTRNSFRMNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR; VC2463;
                                                                                                                                                                                                                                                                                                                                                                      cholerae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
Q96EY0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96EY0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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0
                                                                                                 Strausberg R.;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC002963; AAH02963.1; -
RSSP; P01825; 7FAB.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003600; Ig_like.
InterPro; IPR003606; Ig_WHC.
InterPro; IPR003906; Ig_W.
RAMRT; SW00407; Ig; 5.
SWART; SW00407; IG; 2.
SWART; SW00406; IGV; 1.
SWART; SW00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.8%; Score 51; DB 4; Length 597; llarity 39.1%; Pred. No. 22; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 597;
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
Hypothetical protein.
SEQUENCE 597 AA; 65039 WW; 4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEOUENCE 597 AA; 65274 MW; 2DAFABFB7E055851 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last and
HYPOTHETICAL 65.0 KDA PROTEIN.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00290; IG_MHC; UNKNOWN_3.
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442 GERFTCTVTHTDLPSPLKQTISR 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.8%;
Best Local Similarity 39.1%;
Matches 9; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN LEPA.
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                                                SEQUENCE FROM N.A.
TISSUE-LYMPH, LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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NCBI TaxID=9606;
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Vibrio cholerae.
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GTP-BINDING
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Q96BB9
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2: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
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3: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
5: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
7: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
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9: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
10: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1990.DAT:*
11: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
12: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
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16: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
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17: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*
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19: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1996.DAT:*
                                                                                                                                                                                                                                                                      August 26, 2002, 10:07:02 ; Search time 82.75 Seconds (without alignments) 33.557 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                  OM protein . protein search, using sw model
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Maximum DB seq length: 200000000
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Optimised IdE-CH3	Optimised IgE-CH3	IqE immunoqenic pe	IqE immunoqenic pe	IqE immunogenic pe	IqE immunogenic pe	IgE immunogenic pe	IqE immunoqenic pe	Optimised IGE-CH3	Modified human IqE	Peptide sequence o
SUMMARIES	AAY80077	AAY79999	AAY80019	AAY80083	AAY80020	AAY80081	AAY80080	AAY80084	AAY79998	AAY91212	AAY68602
DB	21	21	21	21	21	21	21	21	21	21	21
% Query Match Length DB	25	25	45	45	46	57	62	63	25	25	25
% Query Match	100.0	77.8	77.8	77.8	77.8	77.8	77.8	77.8	9.69	9.69	9.69
Score	135	105	105	105	105	105	105	105	94	94	94
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IgE immunogenic pe Modified MVF Th ep Modified MVF Th ep Modified MVF Th ep Peptide sequence o IgE-CH3 domain ant	fied Linmu fied	Peptide sequence o IgE immunogenic pe IgE immunogenic pe IgE immunogenic pe IgE immunogenic pe IgE-CH3 domain ant	immunogeni epitope/mo ide sequen imised IgE- immunogeni immunogeni	コケッタグひにゅ
AAY80014 AAY91215 AAY91216 AAY91217 AAY868604 AAY80007	AAY91218 AAY68605 AAY80011 AAY91213 AAY91214	AAY68603 AAY80016 AAY80010 AAY80013 AAY80015	AAY80012 AAY91219 AAY80000 AAY80018 AAY80018 AAY800178	AAY 24097 AAY 29095 AAB 06208 AAR 33067 AAR 90001 AAR 3324 AAR 42620 AAR 33304
21 21 21 21 21 21	217 21 21 21 21 21 21 21 21 21 21 21 21 21	55555	221221	221 221 221 221 24 14
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ALIGNMENTS

Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobelic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-antimatic; asthma; anaphylaxis; dermatitis. Optimised IgE-CH3 domain antigen peptide for horse IgE. ¥. AAY80077 standard; Peptide; 25 (UNBI-) UNITED BIOMEDICAL INC. 99WO-US13959. 98US-0100287. 15-MAY-2000 (first entry) Wang CY, Walfield AM; WPI; 2000-160578/14. Equus caballus WO9967293-A1 21-JUN-1999; 20-JUN-1998; 29-DEC-1999 Synthetic. AAY80077; AAY80077

antigenic peptide from the CH3 domain of immunoglobulin E, fusions immunization against allergy $\,$

New

Gaps

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specific for a target effector site on the epsilon-heavy chain of IgE, and soo preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (1) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (1) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. NAY79994 to AAY80084 represent amino coil sequences used in the exemplification of the present invention.
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Pred. No. 1.1e-09;
4; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY80019 standard; Peptide; 45 AA.
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72.0%;
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Best Local Similarity 72.0°
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 135; DB 21;
100.0%; Pred. No. 1.9e-14;
ive 0; Mismatches 0;
                           Claim 1; Page 146; 155pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                             25 AA;
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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and
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    Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention.
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Pred. No. 2.2e-09;
4; Mismatches 3;
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                                                                                                                                                                                                                        77.8%; 5
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Best Local Similarity 72.0
Matches 18; Conservative
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antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. RAY79994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention.
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       Length 45;
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       Score 105; DB 21;
Pred. No. 2.2e-09;
                                                                                                                                                                                                                                                                                                                      IgE immunogenic peptide conjugate SEQ ID NO:27.
                                          4; Mismatches
                                                                                                 Claim 14; Page 77; 155pp; English
                                                                             1 CGETYKSTVSHPDLPREVVRSIAKC 25
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       77.8%;
72.0%;
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Query Match //.84
Best Local Similarity 72.04
Matches 18; Conservative
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Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobulic; immunoglimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylactic; dermatitis.
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                   AAY80080 standard; Peptide; 62 AA.
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                                              AAY80081 standard; Peptide; 57 AA.
                      1 CGETYKSTVSHPDLPREVVRSIAKC 25
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                                  Immunoglobulin E; 1gE; epsilon heavy chain; antigenic; antigen; fimmunoglobenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-ansthmatic; asthma; anaphylaxis; dermatitis.
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igE immunogenic peptide conjugate SEQ ID NO:91.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Page 77; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY79998 standard; Peptide; 25 AA.
                                                                                                                                                                                                                                                                                                           (UNBI-) UNITED BIOMEDICAL INC.
                                                                                                                                                                                                                                                                       98US-0100287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Conservative
                                                                                                                                                                                                                                                                                                                                               Walfield AM;
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-160578/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 AA;
                                                                                                                                                             WO9967293-A1
                                                                                                                                                                                                                                                                         20-JUN-1998;
                                                                                                                           Unidentified
                                                                                                                                                                                                                                   21-JUN-1999;
                                                                                                                                                                                                 29-DEC-1999
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                                                                                                                                                                                                                                                                                                                                               Wang CY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and soo preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Promiscuous T-cell epitope, measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic; Plasmodium falciparum; circumsporozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified human IgE CH3 domain, SEQ ID NO:92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 21; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY91212 standard; peptide; 25
                                                                                                                                                                               UNBI-) UNITED BIOMEDICAL INC
                                                                                     98US-0100287.
99WO-US13959.
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                                                                                                                                                                                                                                                                         Wang CY, Walfield AM;
                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-160578/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 AA;
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Gaps

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Indels

Length 25;

Score 94; DB 21; Le Pred. No. 6.1e-08;

69.6%; 64.0%;

4; Mismatches

Conservative

Best Local Similarity Matches 16; Conserv

Query Match

1 CGETYKSTVSHPDLPREVVRSIAKC 25

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WPI; 2000-160564/14.
W09966957-A2
   21-JUN-1999;
     :0-JUN-1998;
 29-DEC-1999
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25 AA;

Sequence

á qq The invention relates to novel promiscuous T helper cell epitopes (Th), and minuogenic peptides compitising the Th epitopes and peptide immunogenic containing them, are used to induce a T helper cell response, containing them, are used to induce a T helper cell response, containing them, are used to induce a T helper cell response, containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesteryl ester transport containing them, are used to induce a protein and/or transport protein immunogens may be used for prevention and/or transment of infections (HIV, foot and-mouth lidease or malaria); for cancer immunostariation); for contraception, retenant of hormone (LMRH) for contraception, retenant of a promiscous immunogean immunostariation); for prompting the protein of animals; or for treating allegies or arteriosclerosis. Incorporation of a promiscous capacity to induce a strong T helper cell-mediated immune cell mentocastration); for prompting the per cell-mediated immune cell mentocastration); for prompting the per cell-mediated immune cell mentocastration; in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune cell mentocastration; and sequences subjects) and AN91124-v91134 are participated and AN912125 and AN91125. The performance of the mentocastration in production of antiboder-derived T helper cell-mediated mentocastration and any participates based on the MAY9116-v9116, and AN9118, and AN91118, and any periode AN9118, and AN91118, and AN91118, and any periode AN9118, and AN91118, and AN911 epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis Example 6; Page 40; 129pp; English. antigenic site, for immunization or human immune deficiency virus (UNBI-) UNITED BIOMEDICAL INC. 99WO-US13975. 98US-0100412

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helper T cell epitope; peptide immunogen; LHRH;
luteinising hormone-releasing hormone; spermatogenesis; ovulation;
oestrus; sexual development; sex hormone; promiscuous T helper epitope;
vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
breast cancer; endometriosis; boar taint; meat quality; immunocastration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes peptide immunogens comprising a synthetic helper T cell (Th) epitope and a target antigen, luteinising hormone-releasing hormone (LHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, oestrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast, also endometriosis); to prevent boar taint (and improve meat quality) and for immunocastration. The present sequence appears in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide immunogen containing luteinising hormone-releasing hormone antigen site and helper {\tt T} cell epitope, for e.g. contraception and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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64.0%; Pred. No. 6.1e-08;
ive 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 92; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Peptide sequence of the invention.
                                                                                                                                                                                               AAY68602 standard; peptide; 25 AA.
||||||:| |:|| ||| ::|| ||
| cgetygsrvthphlpralmrsttkc 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||||:| |:|| ||| ::|| ||
| cgetygsrvthphlpralmrsttkc
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Best Local Similarity 64.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
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                                                                                                                                                                                                                                                                    AAY68602;
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Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic; Plasmodium falciparum; circumsporozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis
                                                     Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 98-99; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or human immune deficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UNBI-) UNITED BIOMEDICAL INC.
                22-MAY-2000 (first entry)
                                                                                                                                                                                                                                                      Chimeric - Measles virus.
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                                                                                                                                                                                                                                                                                                             WO9966957-A2.
                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-1999;
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                                                                                                                                                                                                                                                                         Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang CY;
The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-ashmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, acathma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and
                                                                                                                                                                                                                                              immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     maximize cross reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigenic peptide from the CH3 domain of immunoglobulin E, fusions
                                                                                                                                                                                                                              Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
                                                                                                                                                                                         IgE immunogenic peptide conjugate SEQ ID NO:21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Page 76; 155pp; English.
                                                                   AAY80014 standard; Peptide; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunization against allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNBI-) UNITED BIOMEDICAL INC.
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                                                                                                                                                15-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Walfield AM;
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                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                                                          AAY80014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang CY,
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                                12
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                                              AAY80014
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98US-0100412. 99WO-US13975.

- Homo sapiens.

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Interclude (HWY, 1007-and mouth uisease of matalal); for canterious (HWY, 1007-and mouth uisease of matalal); for cantraception, treatment of hormone releasing hormone (LHRH) for contraception, treatment of hormone—

Comproves capacity for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous treating allergies or arteriosclerosis. Incorporation of a promiscuous of the fortional in genetically diverse subjects) into an immunogen in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target on tigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AAY91121 represents a promiscuous T helper epitope from the measles virus F (MVF) protein and sequences AAY9112-Y91142, AAY9125 and AAY9124 represents a promiscuous T hepitope. Crom hepatitis B virus (HWY) surface antigen, and sequences antigenic peptides comprising an LHRH sequence joined to a promiscuous The pitope. AAY91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptides comprising sometostatin and a Th epitope. Sometostatin jimmunogens may be used to promote growth in livestock. AAY91208 is a man of CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 attigenic peptides which may be used to prevent HIV infection of T cells. AAY90215 is a modified version of a human IgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3 antigenic peptides which may be used in the treatment of allergies. AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) VPI capsid protein and AAY91221-Y91222 comprise this peptide and a Th
The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesteryl ester transport protein (CETP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer
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Gaps

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Score 94; DB 21; Length 42; Pred. No. 1.2e-07; 1; Mismatches 5; Indels

69.6%; 64.0%;

Query Match
Best Local Similarity 64.0°
Matches 16; Conservative

4; Mismatches

1 CGETYKSTVSHPDLPREVVRSIAKC 25

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||||||:| |:|| ||| ::|| ||
18 cgetygsrvthphlpralmrsttkc

AAY91215 standard; peptide; 42 AA.

RESULT 13

AAY91215

AAY91215;

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epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS antigen and an WNF The epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a CETP peptide and a Th epitope which may be used to prevent or treat are teriosclerosis and cardiovascular disease. AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising MNH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention *along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a helper cell response, specifically against Plasmodium falciparum, cholesteryl ester transport protein (CETP) or HIV epitopes, but more generally against any pathogen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigon; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic; eholesteryl ester transport protein; anti-antivicit; corpside the protein; anti-antivicit; corpside the protein; anti-antivicit; corpside the protein; anti-antivicities of the protein; anti-antivicities of the protein anti-antivicities.
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                              69.6%; Score 94; DB 21; Length 42; 64.0%; Pred. No. 1.2e-07; ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:96.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY91216 standard; peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGETYKSTVSHPDLPREVVRSIAKC 25
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.0'
Matches 16; Conservative
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Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                        42 AA;
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                                                                                                                                                                                                                                                              Invention.
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immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunoreactive self-antigen or tumour antigen. The action of luteinising hormone clause and be used for prevention treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of luteinising hormone classing hormone (HIRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and dependent cancer, prevention of boar taint in meat, and dependent cancer, prevention of boar taint in meat, and immunosatration); for promoting the growth of animals; or for for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong Thelper cell-mediaced immune response, resulting in production of antibodies against a target antigen. The an replace carrier proteins and pathogen-destried Thelper coll mediaced immune tresponse, resulting in production of antibodies against a target antigen. The nar replace carrier proteins and pathogen-destried Thelper coll mediaced immune tresponse, resulting in production of antibodies against a target antigen. The protein and avayllate (HWF) surface antigen, and sequences avayllate (HWF) surface antigen, and sequences avayllated version and avayllated and avayllated and avayllated and antigenic peptides comprising an LiHR sequence joined to a promiscuous Theptope. Avayllated carrier and pathogens and pathogens and avayllated version of a man antigenic peptides antigenic peptides which may be used to prevent HIV immunogens may be used to promote growth in liveston, and avayllated version of a mediace and avayllated version of a mediace for immunogens may be used in a malaria vaccine. Avayllate and an antigenic peptides which may be used in the treatment of allergies of immunogens man and avayllated fervived from foot and mouth disease virus (FWPV) vpl capsid protein and Avayllate fervived from foot and mouth disease
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Matches 16; Conservative
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cholesteryl ester transport protein; anti-arteriosclerotic.

Chimeric - Measles virus. Chimeric - Homo sapiens.

99WO-US13975. 98US-0100412 (UNBI-) UNITED BIOMEDICAL INC

WPI; 2000-160564/14.

New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the The pitopes of the invention along with B cell epitopes. The The pitopes and peptide immunogens containing them, are used to induce a T helper cell response.

Containing them, are used to induce a T helper cell response.

Containing them, are used to induce a T helper cell response.

Specifically against Plasmodium falciparum, cholesteryl ester transport protein (CETP) or HIV epitopes, but more generally against any pathogen, mannorcherapy; for inhibition of the action of luteinising hormone classing hormone (LIRH) for contraception, treatment of hormone-classing hormone (LIRH) for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous in (Innuctional In genetically diverse subjects) into an immunocation of mingroves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target ceptiopes. Sequence AAY9112 represents a promiscuous T helper ceptiope.

Comprises capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target of the personse. resulting in production of antibodies against a target ceptiopes. Sequence AAY9112 represents a promiscuous Thelper ceptiope.

Comprises Sequence AAY9112 represents a promiscuous Theptope.

Comprises and AAY9124-Y9136 represents a promiscuous The pitope.

AAY91126 and AAY9127 and AAY91201 represents a promiscuous The pitope.

Comprising an LiMH sequence Johned to a promiscuous The pitope.

AAY91144-Y91155 are synthetic epitopes derived from this Hay to a peptides and yay91201 septide used to the pitope.

Comprising an LiMH sequence of other any per used to prevent HIV infection of T cells. AAY91201 seminor are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAX91258-Y91253 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine.
AAY91198 and AAY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of Example 6; Page 99; 129pp; English.

Gaps ; 0 which may optionally be used in the $% \left(1\right) =\left(1\right) +\left(1\right)$ Length 42; Query Match 69.6%; Score 94; DB 21; Length 42 Best Local Similarity 64.0%; Pred. No. 1.2e-07; Matches 16; Conservative 4; Mismatches 5; Indels 42 AA; Sequence SSXS

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1 CGETYKSTVSHPDLPREVVRSIAKC 25 ||||||:|||:|| ||| ::|| || 18 cgetyqsrvthphlpralmrsttkc 42 qq ò

Search completed: August 26, 2002, 10:07:02 Job time: 228 sec

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Pred. No. 8e-09;
4; Mismatches
US-08-399-106A-7
US-08-433-105A-7
US-08-434-865A-7
US-09-049-672A-1
US-09-049-672A-1
US-09-332-915-2
US-08-630-172-20
US-08-630-172-19
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US-08-875-533-41
US-08-875-533-41
US-08-875-533-68
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STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZID.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 95, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Xi
TITLE OF INVENTION: IMMUNOGENS
ITILE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGETYQSRVTHPHLPRALMRSTTKC 25
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NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REPERENCE/DOCKET NUMBER: 1151-
TELECOMMUNICATION INFORMATION:
TELEFRAK: 212-754-6849
INFORMATION FOR SEQ ID NO: 95:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGETYKSTVSHPDLPREVVRSIAKC
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CLASSIFICATION: 424
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64.08;
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LENGTH: 25 amino acids
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Best Local Similarity 64.0
Matches 16; Conservative
     ; MOLECULE TYPE: peptide US-09-100-414B-95
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COMPUTER READABLE FORM:
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Sequence 95, Appl
Sequence 98, Appl
Sequence 99, Appl
Sequence 100, Appl
Sequence 101, Appl
quence 101, Appl
uence 101, Appl
uence 101, Appl
nence 96, Appl
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ne 97, Appl
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17.865 Million cell updates/sec
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54, Appl
56, Appl
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Patent No. 5284931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 20,
                                                                                                                                                                                                August 26, 2002, 10:05:19; Search time 34.18 Seconds
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-100-414B-99

US-09-100-414B-109

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US-09-303-323-99

US-09-303-323-99

US-09-100-414B-101

US-09-100-414B-96

US-09-100-414B-96

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US-09-303-323-97

US-09-303-323-97

US-09-303-323-97

US-09-303-323-97

US-09-303-323-97

US-08-323-539D-54

US-08-322-539D-56

US-08-322-539D-19

US-08-232-539D-19

US-08-232-539D-19

US-08-232-539D-19
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-08-466-163B-1
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1 CGETYKSTVSHPDLPREVVRSIAKC
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5284931-11
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Minimum DB seq Maximum DB seq

Database :

Result Š.

Title: Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

Searched:

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Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-100 414B-99
Sequence 99, Application US/09100414B
Fatent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: INMUNOGENS
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
SOFTWARE: Word 97

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
FELECOMMUNICATION INFORMATION:
FELEPRONE: 212-754-6849
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: APPLICATION
US-09-100-414B-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTY: U.S. COMPUTER: U.S. COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-UNE-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPHONE: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.6%;
64.0%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: peptide US-09-100-414B-99
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                     Sequence 95, Application US/09303323
Fatent No. 6228987
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOCENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 98, Application US/09100414B
Fatent No. 6025468
GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNOGENS
TITLE OF INVENTION: IMMUNOGENS
OORRESPONDENCE ADDRESS:
ADDRESSEE: MOTGAN & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MATLA H. LIN
REGISTRATION NUMBER: 29.323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECHONICATION INFORMATION:
TELECHONE: 212-758-4800
TELEFRAX: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
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AEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-751-6849 INFORMATION FOR SEQ ID NO: 95:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
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Best Local Similarity 64.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide US-09-303-323-95
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ZIP: 10154-0054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 3(CLASSIFICATION:
                                                                                                                                                                                                                                                                                                          USA
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US-09-100-414B-98
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                                      US-09-303-323-95
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64.0%; Pred. No. 1.5e-08;
Live 4; Mismatches 5; Indels
                                    COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30 APR-1999
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELEPHONE: 212-758-480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue
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ZIP: 10154 -0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGETYKSTVSHPDLPREVVRSIAKC 25
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APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Maria H. Lin
REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 64.09
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 345 Par
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-303-323-99
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Pred. No. 1.5e-08;
4; Mismatches 5; Indels
    Indels
    5.
    4; Mismatches
                                                                                                                                                                                        Sequence 100, Application US/09100414B
Fatent No. 6025468
GENERAL INFONDATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: INMUNOGENS
TITLE OF INVENTION: IMMUNOGENS
WINMER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. LIN
REGISTRATION NUMBER: 29,323
REGISTRATION NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       E: Morgan & Finnegan, L.L.P.
345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                       STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: NY
COUNTRY: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                    18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                           1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGETYKSTVSHPDLPREVVRSIAKC 25
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Sequence 98, Application US/09303323

Patent No. 6228987

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.6%;
64.0%;
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LENGTH: 42 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.0°
Matches 16; Conservative
Matches 16; Conservative
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MOLECULE TYPE: peptide
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10154-0054
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Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
              GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                         COUNTER TO JOSA

ZIP: 10154-0054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: WORD 97

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFCATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Maria H. Lin
RECISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPOMNUNICATION INFORMATION:
TELEPAX: 212-751-6849
INFORMATION FOR SED ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids

"WIND: AMINO acids
"WIND: AMINO acids
"WIND: AMINO acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGETYKSTVSHPDLPREVVRSIAKC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.6
Best Local Similarity 64.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-09-100-414B-101
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ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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TOPOLOGY: linear
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Patent No. 6025468
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                                                                                                                                                                               CITY: New
STATE: NY
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: N
STATE:
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                                                                                                                                           Score 94; DB 4; Length 42;
Pred. No. 1.5e-08;
....a+rhes 5; Indels
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                                                                                                                                                                                                                                                           RESULT 8
US-09-303-323-100
Sequence 100, Application US/09303323
Sequence 100, Application US/09303333
Patent No. 6228987
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTGAN & Finnegan, L.L.P.
STREET: 345 PATK Avenue
CITY: New York
STATE: NY
                                                                                                                                                          Query Match 69.6%; Score 94; DB Best Local Similarity 64.0%; Pred. No. 1.5e Matches 16; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT • 9
US-09-100-414B-101
; Sequence 101, Application US/09100414B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                          1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGETYKSTVSHPDLPREVVRSIAKC 25
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TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 100:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 64.09
                   LENGTH: 42 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
SEQUENCE CHARACTERISTICS
                                   ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-100
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22 CGETYQSRVTHPHLPRALMRSTTKC 46

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Pred. No. 1.7e-08;
4; Mismatches 5
                                                                                                                Sequence 97, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 96, Application US/09303323

Patent No. 6228987

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL LHRH PEPTIDE

TITLE OF INVENTION: INMUNOGENS

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/09/100,414B
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COUNTY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 CGETYQSRVTHPHLPRALMRSTTKC 46
                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 1.
TELECOMMUNICATION INFORMATION
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.6%;
64.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 46 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 69.6
Best Local Similarity 64.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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Pred. No. 1.6e-08;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.6%; Score 94; DB 3; Length 46; 64.0%; Pred. No. 1.7e-08; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 96, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNOGEN
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STRRET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCETARIAN SISTEM.
SUFTRARE: WOR'D 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
                                                                                              REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1151-4157
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APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                            TELEFAX: 212-751-664-7
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 11.
TELECOMMUNICATION INFORMATION: 212-758-4800
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64.0%;
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.0%
Matches 16; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-09-303-323-101
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10154-0054
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STATE:
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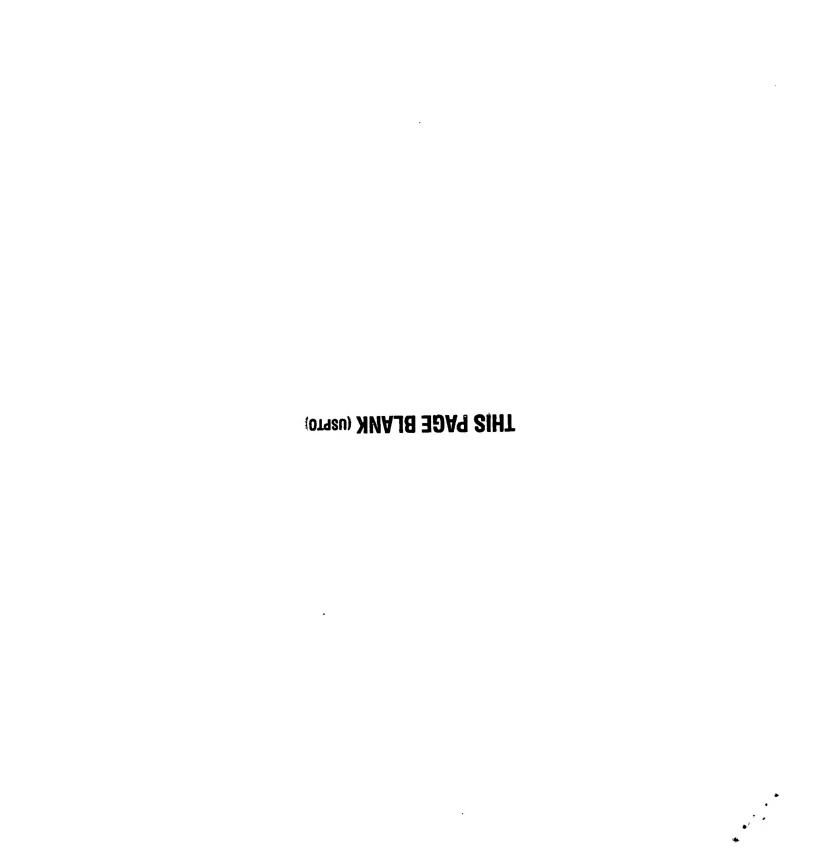
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                                                                                                          Length 46;
                                                                                                                                                      Indels
                                                                                          Score 94; DB 4; Len
Pred. No. 1.7e-08;
                                                                                                                                                                                                                                                                                                                                   SQUENCE 102, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
FITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STRATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER: IBM PC COMPATIBLE
COMPUTER: NOTG 97
CURRENT APPLICATION DATA:
ATTORNEY ARE NOTG 97
CLASSIFICATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEFRANT OF COMPATION INFORMATION:
TELEFRANT ON TO STATE OF THE NUMBER: 1151-4157
TELEFRANT STATE OF THE NUMBER: 1151-4157
TELEFRANT STATE OF THE NUMBER: 1151-4157
                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: August 26, 2002, 10:05:19 Job time: 125 sec
                                                                                                                                                                                                1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                    22 CGETYQSRVTHPHLPRALMRSTTKC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGETYKSTVSHPDLPREVVRSIAKC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 102:
                                                                                                          Query Match
Best Local Similarity 64.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.09
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                          ; MOLECULE TYPE: peptide US-09-303-323-97
      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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US-09-100-414B-102
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Pred. No. 1.7e-08;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 97, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: IMMUNOGENS
INTRE OF INVENTION: IMMUNOGENS
ORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
O9/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MARIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHNONE: 212-758 4800
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1151-4157
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-41:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-758-4800
TELEFAX: 212-751-6849
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC Windows
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Best Local Similarity 64.0%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                             homo sapien
mus musculu
mus musculu
  gallus gall
lytechinus
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homo sapien
                                                                                        xenopus lae
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mus musculu
                               caenorhabdi
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig epsilon chain C region.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.; "Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hellman L., Pettersson U., Bennich H.; "Characterization and molecular cloning of the mRNA for the heavy (epsilon) chain of rat immunoglobulin E."; Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
MEDLINE=83182019; PubMed=6820340;
Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
"A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, identification, and DNA sequence.";
DNA 1:335-343(1982).
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Immunoglobulin domain; Immunoglobulin C region.
NON_TER 1 1 1 1 1 CONFLICT 168 168 R -> N (IN REF. 2)
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MUC_CHICK
KPC1_LYTP1
ACLY_CAEEL
FZD8_XENLA
OC90_CAVPO
RS20_HUMAN
RS20_XENLA
RS20_XENLA
RS20_DROME
HB2F_MOUSE
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HB2K_MOUSE
HB2S_MOUSE
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MEDLINE-83064537; PubMed-6292865;
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MEDLINE-82174576; PubMed = 6803238;
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  August 26, 2002, 10:17:02; Search time 24.08 Seconds (without alignments) 40.199 Million cell updates/sec
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              GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                           Score 122; DB 1; Length 429;
Pred. No. 1.6e-10;
0; Mismatches 1; Indels
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  P -> L (IN REF. 2).
D2970B34EF8A72B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chain cDNA.";
Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
                                                                                                                                                                                                                                                                                          EPC_MOUSE STANDARD; PRT; 421 AA. P06336; P01856; 21-JUL-1986 (Rel. 01, Created) LFB2-1996 (Rel. 33, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Ig epsilon chain C region.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 4.
SMART; SM0410: IG_like; 2.
SMART; SM0407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 3.
  308 P
48671 MW;
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                                                                           Query Match 84.1%;
Best Local Similarity 95.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90
197
304
421
75
180
285
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
308 3
429 AA;
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CONFLICT
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MEDLINE-83001945; PubMed-6288268;
MAX E.E., Battey J., Ney R., Kirsch I.R., Leder P.;
"Duplication and deletion in the human immunoglobulin epsilon genes.";
Cell 29:691-699(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
(In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.1-36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-83168897; PubMed-6300763; Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K., Kikuchi M., Sugino Y., Nishida Y., Honjo T.; "Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon chain cDNA."; Nucleic Acids Res. 11:719-726(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE-84236029; PubMed-6234164;
Flanagan J.G., Rabbitts T.H.;
"The sequence of a human immunoglobulin epsilon heavy chain constant
region gene, and evidence for three non-allelic genes.";
EMBO J. 1:655-660(1982).
                                                                                                                                                                                                                                                                                                                                                Gaps
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SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.
MEDLINE-83065234; PubMed-6815656;
Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDIMEd-6327276; MEDILINE-84207910; PubMed-6327276; UGda S., Nakai S., Nishida Y., Hisajima H., Honjo T.; Ucda S., Nishida Y., Hisajima H., Honjo T.; "Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudogene that lacks introns.";
                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                 Score 98; DB 1; Length 421;
Pred. No. 5.2e-07;
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                  N-LINKED (GLCNAC...) (1
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428 AA
       SIMILARITY
                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND)
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                                                                                                                                                                                                                                                                                                                                                                                                                   2 GEGYQSRVDHPHFPKPIVRSITK 24
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                                                                                                                                                                                                                                 MW.
                                                                                                                                                                                                                                                                                              Query Match 67.6%;
Best Local Similarity 82.6%;
Matches 19; Conservative (
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43
72
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84
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84
95
166
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361
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46
264 AA;
              SEQUENCE FROM N.A.
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1121
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P15979;
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TRANSMEM
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DISULFID
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CARBOHYD
SEQUENCE
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
RT1 class II histocompatibility antigen, D-1 beta chain precursor.
 Be'l L.O., Gould H.J.; "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
M -> L (IN REF. 2, POSSIBLY DUE TO
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0
                                                                                                                                                                                                                                                                                                         Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                            INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 80; DB 1; Length 428;
Pred. No. 0.00023;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR_003885,
25C4CA072AA558A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 AA.
                                                              Padlan E.A., Davies D.R.; "A model of the F=C= of immunoglobulin E."; Submitted (JUL-1993) to the PDB data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLYMORPHISM)
                                                                                                                                                                                         EMBL; L00022; AAB59424.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GEGYQSRVDHPHFPKPIVRSITK 24
|| || || || || || || || 3
294 GETYQCRVTHPHLPRALMRSTTK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                      InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 4. SMART; SMO407; IGC1; 4. PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.2%;
Best Local Similarity 60.9%;
Matches 14; Conservative
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                                                                                                                                                                                                   PIR; A02142; EHHU.
PIR; A22771.
PIR; A33195; A23195.
PDB; 11GE; 15-JUL-92.
MIM; 147180; -
                                                                                                                                                                                                                                                                                                                                          14
105
85
85
121
121
193
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209
405
                                                      3D-STRUCTURE MODELING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428 AA;
                                                                                                                                                                                                                                                                                                                     3D-structure
Beil L.O.,
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1D HB2D_RAT

AC P18211;

DT 01-NOV-199

DT 15-JUL-199

DE RT1 class

DS Rattus nor

CC Mammalla;

OC Mammalla;

OX NCBI_TAXID
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                          coding for the RT1.D beta I
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15-JUL-1999 (Rel. 18, Last annotation update)
Class I histocompatibility antigen, F10 alpha chain precursor (B-F
histocompatibility F10 antigen) (B-F-beta-IV) (B12).
Gallus gallus (Chicken).
                                                                                          chain.";
Nucleic Acids Res. 18:4598-4598(1990).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
158F357355177DA1 CRC64;
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STRAIN-B12; ITSSUE-Liver;
MEDLINE-89030642; PubMed-3141149;
Guillemot F., Billault A., Pourquie O., Behar G., Chausse A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Pred. No. 2.4;
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EXTRACELLULAR BETA-1.
EXTRACELLULAR BETA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONNECTING PEPTIDE.
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHC II; Transmembrane; Glycoprotein; Signal.
STRAIN=LEWIS FAMILIARIS; TISSUE=Bone marrow;
MEDLINE=90356406; Pubmed=2388838;
Syha-Jedelhauser J., Reske K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                        "Sequence of rat cDNA clone pLR beta 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X53054; CAA37221.1; -.
PIR; S10989; S10989.
HSSP; P13760; 2SEB.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003597; Ig_cl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
Pfam; PF000869; MHC_II_beta; 1.
Probom; PD000328; MHC_II_beta; 1.
SMART; SM00407; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Created)
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29876
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Best Local Similarity 4/...
8: Conservative
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226
248
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200
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Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                      PKC SUBFAMILY.
                                                            STRAIN-BRISTOL N2;
                                                  SEQUENCE FROM N.A.
                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phorbol-ester
                                                                                                                                                                                                                        Miwa J.;
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NP_BIND
BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                         CLASS I HISTOCOMPATIBILITY ANTIGEN, F10
                 class II beta genes are closely linked to the class I genes and the nucleolar organizer."; EMBO J. 7:2775-2785(1988).
Zoorob R., Kreibich G., Auffray C.;
"A molecular map of the chicken major histocompatibility complex:
                                                                             Kroemer G., Zoorob R., Auffray C.;
Structure and expression of a chicken MHC class I gene.";
Immunogenetics 31:405-409(1990).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMUNE SYSTEM.
-i- SUBBNIT: DIAMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
P -> PDREGSSSST (IN REF. 2).
430DCCF8091B69A4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                         CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPC1_CAEEL STANDARD; PRT; 704 AA. P34722; 01-FBB-1994 (Rel. 28, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Protein kinase C-like 1 (EC 2.7.1.-) (PKC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 6.2;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Signal.
                                                            SEQUENCE FROM N.A.
MEDLINE-90316612; Pubmed-2370087;
                                                                                                                                                                                                                                    EMBL; X12780; CAA31272.1; --
EMBL; M31012; AAA48947.1; --
PIR; S01172; HLCH84.
PIR; A45846; A45846.
HSSP; P03889; 1HSA.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C.1.
InterPro; IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38246 MW;
                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; 1g; 1.
Pfam; PF00129; MHC_I; 1.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGG1; 1.
PROSITE; PS00290; IG_MHC; 1.
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345 AA;
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                                                                                                                                     Gaps
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MEDLINE-80012837; PubMed-113776;
Rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE-8020255; PubMed-6769752;
Obata M., Yamawaki. Kateoka Y., Takahashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma I heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-80045036; PubMed-115593; Manojo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.; "Cloning and complete nucleotide sequence of mouse immunoglobulin
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MEDLINE-73008889; PubMed-5073237;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Blochem. J. 126:837-850(1972).
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                                                                                        DB 1; Length 704;
  137 MISSING (IN ISOFORM TPA-1B).
80298 MW; C44F2E25F58057E3 CRC64;
                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                 324 AA
                                                                                   33.4%; Score 48.5; D
37.9%; Pred. No. 15;
live 2; Mismatches
                                                                                                                                                                                                  2 GEGYQSRVD-----HPHFPKPIVRSITKC 25
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J. Blol. Chem. 253:6068-6075(1978).
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Mus musculus (Mouse).
                                                                                                          Best Local Similarity 37.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Cell 18:559-568(1979)
                      704 AA;
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P01868;
VARSPLIC
SEQUENCE
                                                                                        Query Match
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ID GCCL_MOUSE

DT 21-JUG

OC Mamma

CC Mamma

RR MEDLII

RR MEDLII

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Gaps
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutenesia; Rodentia; Sciurognathi; Muridae; Musing, NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A. MEDLINE-80045036; PubMed=115593; MEDLINE-80045036; PubMed=115593; Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.; Takahashi N., Mano Y.; "Cloning and complete nucleotide sequence of mouse immunoglobulin "Cloning and complete.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.; "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                               PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (WITH A LIGHT CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REMOVED POST-TRANSLATIONALLY
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N -> D (IN REF. 3).
A338812F3D1F2C93 CRC64;
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HINGE.
CH2.
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SEQUENCE OF 323-366 FROM N.A.
MEDLINE-82115295; PubMed-6799207;
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193 GKEFKCRVNSAAFPAPIEKTISK 215
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39.1%;
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_cl.
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324
276
278
35704 E
; V00793; CAA24175.1;
; V00795; CAA24176.1;
A02159; GIMS.
                                                         HSSP; P01842; 7FAB.
GlycoSuiteDB; P01868; -.
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324 AA;
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SMART; SM00407; IGC
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hes 9; Conserv
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P01869;
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38, Last annotation update)

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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
    15-JUL-1999 (Rel. 38, Last and gamma-2A chain C region.
                         Rattus norvegicus (Rat)
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DER2_HUMAN
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                                                                                  Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains."

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

-I. ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' SND, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
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Rogers J., Chol E., Souza L., Carter C., Word C.J., Kuehl M., Elsenberg D., Wall R.; "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains."; cell 26:19-27(1981).
                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00407; TGc1; 2.
PROSITE; PS00299; IC_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative spilcing; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (WITH A LIGHT CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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Pred. No. 9.9;
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4CC88343B7A1CE27 CRC64;
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(Rel. 17, Last sequence update)
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                                                                           MEDLINE-82222190; PubMed-6283537;
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39.1%;
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MGD: MGI:96446; 1gh-4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
Pfam; PF00047; 1g; 3.
                                                                 SEQUENCE OF 1-44 FROM N.A.
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Best Local Similarity
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01-FEB-3991
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P20760;
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DOMAIN
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Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                              Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
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bustaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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Mei G., Yu W., Gibbs R.A.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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TISSUE-Dermal papilla;
TIKeda A., Yamashita M., Yoshimoto M.;
"Molecular cloning of a dermal papilla derived gene.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EBEA136A9DE01EDB CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dermal papilla derived protein 2 (My021 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain; Immunoglobulin C region
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PIR; PS0019; PS0019.
HSSP; P01842; 7FAB.
LINCEPPO; IPR0033006; Ig_MHC.
LINCEPPO; IPR003597; Ig_C1.
                                                                                                                                     MEDLINE-89232738; PubMed-3149946;
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| 191 GKTFKCKVNSGAFPAPIEKSISK 213
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SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
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102
105
107
196
300
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Best Local Similarity
Matches 9; Conserv
                                                                                                           SEQUENCE FROM N.A.
                                                        NCBI_TaxID=10116;
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                                                                                                                   Mismins 2.1.4.3.1.5 Fubmed-112.0100.8

Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaler B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.;

"Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
Genome Res. 11:422-435(2001).

-! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                       Mao Y.M., Xie Y., Mu Z.M., Li Y., Huang Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                808FAED86A9CD98E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative superoxide reductase (EC 1.18.96.1) (SOR).
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(IN REF. 4).
(IN REF. 4).
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MEDLINE-96337999; PubMed-8688087;
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                                                                                                           MEDLINE=21154917; PubMed=11230166;
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146
180
211
234
265
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74
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345 AA;
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Best Local Similarity
Matches 14; Conserv
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              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
126
160
191
214
                            TISSUE-Brain;
                                                                                                 TISSUE-Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane
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Q58151;
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                                                                                                                                                              jannaschii";
Science 273:1058-1073(1996).
-!- FUNCTION: USES ELECTRONS FROM REDUCED NADP, BY WAY OF RUBREDOXIN
--- FUNCTION: USES ELECTRONS FROM REDUCED NADP, BY WAY OF RUBREDOXIN
--- AND AN OXIDOREDUCTASE, TO CATALYZE THE REDUCTION OF SUPEROXIDE TO
HYDROGEN PEROXIDE (BY SIMILARITY).
--- CATALYTIC ACTIVITY: Reduced rubredoxin + superoxide + 2 H(+) =
H(2)0(2) + rubredoxin.
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-89345182; PubMed=2762160;
COX G.J., Parker M.D., Babluk L.A.;
"The sequence of cDNA of bovine coronavirus 32K nonstructural gene.";
Nucleic Acids Res. 17:5847-5847(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine coronavirus (strain Quebec).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002742; Desulfoferrodox.
Pfam: PF01880; Desulfoferrodox; 1.
Probom: PD006618; Desulfoferrodox; 1.
Hypothetical protein; Oxidoreductase; Electron transport; Iron; Complete proteome.
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                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE DESULFOFERRODOXIN FAMILY.
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Pred. No. 5.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 AA.
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nes 10; Conservative
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52
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52
101
104
116 AA;
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Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,
Irimura T., Takahashi N., Rato K., Arata Y.;
"0-04ycosylation in hinge region of mouse immunoglobulin G2b.";
J. Biol. Chem. 269:12345-12350(1994).
-i- Prin. O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS
-k. MODIFIED WITH 2 STALIC ACID RESIDUES.
-i- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (B ALLELE).
MEDLINE-82173203; PubMed-6803173;
Ollo R., Rougeon F.;
"Mouse immunoglobulin allotypes: post-duplication divergence of gamma 2a and gamma 2b chain genes.";
Nature 296:761-763(1982).
 There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-80081502; Pubmed-117549;
Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
"Sequence of the cloned gene for the constant region of murine gamma 2b immunoglobulin heavy chain.";
Science 206:1303-1306(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.; "Structure of the constant and 3' untranslated regions of the murine gamma 2b heavy chain messenger RNA."; Science 206:1299-1303(1979).
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (A ALLELE).
MEDLINE-80120716; Pubmed-6766534;
Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
"Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from newborn nouse DNA.";
Nature 283:786-789(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                             ;
                                                                                                                                                                                Length 277;
                                                                                                                                                                                                             2; Indels
                                                                                                                                    D2EEC7BAFB86EA11 CRC64;
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                                                                                                                                                                                Score 46; DB 1;
Pred. No. 14;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 01, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  336 AA
 the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (MPC 11).
MEDLINE-80081501; Pubmed-117548;
                                                                                                                   Nonstructural protein.
SEQUENCE 277 AA; 31896 MW;
                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                31.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last Ig gamma-2B chain C region.
                                                                                       EMBL; X15445; CAA33485.1;
                                                                                                                                                                                                             7; Conservative
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                           2 GEGYQSRVDHPH 13
                                                                                                                                                                                                                                                                      78 GEGFQIKFDNPH 89
                                                                                                      PIR; A34039; MNIH32
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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P01866;
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GCB_MOUSE
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                                                                                                                                                                                                                                                                                                O-LINKED (GALNAC. . .).
REMOVED POSTTRANSLATIONALLY (PROBABLE).
G -> R (IN B ALLELE).
T -> A (IN B ALLELE).
N -> D (IN B ALLELE).
M -> I (IN B ALLELE).
L -> S (IN REF. 2 AND 3).
S -> P (IN REF. 2 AND 3).
I -> T (IN REF. 2 AND 3).
S -> P (IN REF. 2 AND 3).
WHY 7D879662607C356E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seeger K., Harris D., McDougall R.C., Rajandream M.A., Barrell B.G., Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: PORPHYRIN AND HEME BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE UROPORPHYRINGGEN DECARBOXYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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CHAIN).
                                                                                                                                 Immunoglobulin C region; Glycoprotein.
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16-OCT-2001 (Rel. 40, Last annotation update)
Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).
SPCC4B3.05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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HSSP; P01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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(Rel. 40, Last sequ
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                                                                                                                                                                                                                                                                                             105
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Best Local Similarity
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Q9USJ5;
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DCUP_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inouye C., Remondelli P., Karin M., Elledge S.;
"Isolation of a cDNA encoding a metal response element binding protein
using a novel expression cloning procedure: the one hybrid system.";
DNA Cell Biol. 13:731-742(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Metal-response element binding transcription factor 2 (Zinc-regulated factor 1) (ZiRF1) (Metal-response element DNA-binding protein M96)
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97234834; Pubmed-9173905; Remondelli P., Leone A.; Interactions of the zinc-regulated factor (ZiRFI) with the mouse
EMBE; AL132870; CAB60679.1; -.
HSSP; P06132; 1URO.
InterProt; IPRO00257; Uroporphyrngn_decarbxyls.
Pfam; PF01208; URO-D; 1.
PROSITE; PS00906; UROD_1; FALSE_NEG.
PROSITE; PS00907; UROD_2; 1.
Lyase; Decarboxylase; Porphyrin blosynthesis; Heme blosynthesis.
SEQUENCE 370 AA; 41846 MM; 1100FC463733FD89 CRC64;
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87.5%; Pred. No. 18;
tive 1; Mismatches 0; Indels
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InterPro; IPR001965; PHD.
Pfam; PF000628; PHD; 2.
SMART; SM00249; PHD; 2.
DNA-binding; Nuclear protein; Repeat; Zinc-finger; Zinc;
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PHD-TYPE 2.
POLY-LYS.
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MEDLINE=95290093; PubMed=7772254;
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Q02395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fragment).
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MTF2_MOUSE
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Gaps
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0
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                                                                Indels
 42003 MW; 50D2ECD13A5DE817 CRC64;
                                                              13;
                                                            3; Mismatches
                                                              Conservative
373 AA;
                                             Best Local Similarity
Matches 8; Conserv
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1 CGEGYQSRVDHPHFPKPIVRSITK 24 δλ g

23 CGGGYHQLCHTPHIDSSVIDSDEK 46

Search completed: August 26, 2002, 10:17:03 Job time: 699 sec

gallus gall qallus qall

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RC SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;

RAdama M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RA Adama M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RA Adama M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutfon G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Rannon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Bullew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Buttls K.C., Busam D.A., Buttler H., Cadleu E., Center A., Chandra I.,

RA Buttls K.C., Busam D.A., Buttler H., Cadleu E., Center A., Chandra I.,

RA Buttls K.C., Busam D.A., Dattler H., Cadleu E., Center A., Chandra I.,

RA Buttls K.C., Busam D.A., Buttler H., Cadleu E., Center A., Dietz S.M.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Borbon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Burtis N.L., Harvey D., Hehman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Hehman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Hehman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Hehman T.J., Hernandez J.R., Houston K.A.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum R.A.,

Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
                                                031412 gallus gall
046792 gallus gall
095593 gallus gall
095601 gallus gall
0991p6 gallus gall
046788 gallus gall
046789 gallus gall
046790 gallus gall
073901 gallus gall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q991c4 mus musculu
Q96jg0 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropea; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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098188
098191
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P79590
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098193
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Q9nkd7 drosophila
Q90144 drosophila
Q30827 ovis aries
Q31270 rattus norv
Q9tq37 rattus norv
Q9tq55 rattus norv
Q95556 pongo pygma
Q95556 pongo pygma
Q95516 pongo pygma
Q95516 pongo pygma
Q95517 rattus norv
Q95517 rattus norv
Q95518 norociana t
Q95518 nicotiana t
Q947h5 nicotiana t
Q947h5 nicotiana t
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64.724 Million cell updates/sec
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                                                                                                                                                                                  August 26, 2002, 10:16:18; Search time 66.82 Seconds
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                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                 CGEGYQSRVDHPHFPKPIVRSITKC 25
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Listing first 45 summaries
                                                                                                                               OM protein - protein search, using sw model
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Q9TQA7
Q9TQA5
Q99A59
Q95536
Q95SH2
                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Q30827
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_human:*
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sp_bacteriap:*
sp_archeap:*
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sp_phage:*
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length: 2000000000
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145
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sp_mhc:*
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701
217
2245
2245
264
1140
1142
337
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539
539
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Minimum DB seq Maximum DB seq

Database :

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Score

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Result

Q947H5 Q947H4 Q965D2 Q9CZ59

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256 CGEGVKARVSYVSPDPEFTPPVIYSL 281
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                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 CGKGYVSRKDHGH 57
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Best Local Similarity
Matches 9; Conserv
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                                                                                Q9NKD7
                                                                                               Q9NKD7
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Q9NKD7
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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Mervilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Murphy D.M., Nelson D.L.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Spier E., Spradling A.C., Staplecon M., Strong R., Sun F.,

RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Sylrskas R., Tector G., Turner R., Venter E., Wang S., Yao Q.A.,

RA Sylrskas R., Tector G., Yonley K.C., Wu D., Yang S., Yao Q.A.,

RA Sylrskas R., Tector G., Yonley K.C., Wu D., Yang S., Yao Q.A.,

RA Sylrskas R., Tector G., Yonley K.C., Wu D., Yang S., Yao Q.A.,

RA V.J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

R. Johbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT The genome sequence of Drosophila melanogaster.";

R. Science 287.2185-2195-2000;

R. Hybase; FB90013165; Zefring.

B. Rhybase; FB90013165; Zefring.

B. Rhybase; FB90013165; Zefring.

B. SWART; SM00184; RING; Zefring.

SNART; SM00184; RING; Zefring.

SNART; SM00184; RING; Zefring.

SEQUENCE 2421 AA, 269655 MW; 6F1SEF99128F13B0 CRC64;
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STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Watanabe A., Ishikawa A., Nakasumoto M., Matsumoto M., Matsumo A., Mochizuki Y., Nakayama S.; Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium lotti."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62; DB 5; Length 2421; Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-00T-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ņ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGEGYQSRVDH----PHFPKPIVRSI 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 7:331-338(2000).
EMBL; AP003004; BAB51213.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                            42.8%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 || |: |||: |:
211 GPGYMSQQHHPHYPPPV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GEGYQSRVDHPHFPKPI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          098DQ7;
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RAINELY, CN BW SP;

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

CITATION OF SELFORM STATES A CALINER T.T., Baxter E., Blazej R.G.,

Colliker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,

RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,

RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,

RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,

Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Noshrefi A.R., Nixon K., Paoleb J.M., Park S., Ffelffer B., Poon L., Sequeira A.,

RA Alason S., Li P., Lomotan M.A., Mazda P., Weinburg T., Zhang R.,

RA Zieran L.L., Rubin G.M.;

RA Zieran L.L., Rubin G.M.;

Submitted (WAR-2000) to the EMBL/GenBank/DOBJ databases.

R. Submitted (WAR-2000) to the EMBL/GenBank/DOBJ databases.

R. Submitted (WAR-2000) to the EMBL/GenBank/DOBJ databases.

R. Share SMO0181; EGF-11ke.

SMART; SMO0181; EGF-11ke.

SMART; SMO0181; EGF-11ke.

SMART; SMO181; EGF-11ke.

SMART; SMO181; EGF-2; UNKNOWN_6.

R. Wypothetical protein.
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0
                                                01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-700-2001 (TrEMBLrel. 17, Last annotation update)
01-700-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 69.4 KDA PROTEIN.
BG:DS00180:14 OR CG18146.
Drosophila metanogaster (Fruit fly).
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Pterryota: Neoptera: Endopteryota: Diptera: Brachycera: Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=Y, CN BW SP;
MEDLINE-99403001; PubMed-10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celuiker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
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Last annotation update)
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648 AA
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PRT;
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69.2%;
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Ouery Match
Best Local Similarity 52...
Best Good 9, Conservative
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Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
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Matches 8; Conserv
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Q31270
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RATAIN-BERKELEY;
RATAIN-BERKELEY;
RATAIN-BERKELEY;
RA Amanatides P.G., Scherer S.E., High R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Amanatides P.G., Scherer S.E., Ii P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
Apan K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basua A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basua A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basua A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Cawley S., Dalkhe C., Davenpoort C.B., Ecther A., Chandra I.,
RA Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Cherry J.M., Cawley S., Dalkhe C., Davenpoort L.B., Davies P.,
RA Glodek A., Gobriellan A.E., Garry N.S., Gelbart W.M., Glasser K.,
RA Borton K.J., Evangelista C.C., Ferraz C., Ferraz C., Parris M.
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Alali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Mattei B., McIntosh T.C., McLeod M.P.; McPherson D.,
R. Mandel B.E., Kodire C.D., Kraft C., Mortis J., Moshman M.,
Rabon D.R., Woyl M., Wurphy B., Murphy L., Murany D.M., Nelson D.K.,
A Shue B.C., Spradiling A.C., Stapleton M., Stupki M., Palas K.,
Shue B.C., Spradiling A.C., Stapleton M., Stupki M., Wang Z.Y., Wassarman D.A., Weissenbech J.,
R. Sturkas R., Wassarman D.A., Weinschock G.M., Weissenbech J.,
R. Shue B.C., Shadel F.W., Wardy K., Shu B., Shue B., Shade S., Shade M., Shue B., Shong S., Pan M., Shue S., Pollard J., Shan S., Pollard J., Shan S., Pollard J., Shan S., Pollard J., Shan S., Pollard 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SMUULL; LOSF, L.S.
SMART; SM00001; EGF_11ke; 2.
PROSITE; PS01186; EGF_2; UNKNOWN_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OVAR-DOB PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003642; AAF53366.1; -
FlyBase; FBgn0028939; BG:DS00180.14.
Interpro; IRR000561; EGF-11ke.
SMART; SM00181; EGF; 10.
SMART; SM00001; EGF_11ke; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Matches 9; Conservative
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   NCBI_TaxID=7227
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Q30827;
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Q30827
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Robertson K.A., McMaster W.R.;
"Complete structure of a rat RT1 E-beta chain: Extensive conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAT MHC RT1 CLASS II E-BETA CHAIN (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 AA; 28069 MW; 6B21DADB2A4A299D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24707 MW; 1E246E7DBC2AC6B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
STRAIN-FINNISH LANDRACE; TISSUB-BLOOD;
STRAIN-FINNISH LANDRACE; TISSUB-BLOOD;
MEDLINE-96128257; Pubmed-8537127;
Wright H., Redmond J., Ballingall Y.;
"The sheep orthologue of the HLA-DOB gene.";
Immunogenetics 43:76-79(1996).
EMBL; 249879; CAA90036.1;
EMBL; 249880; CAA90036.1;
EMBL; 249880; CAA90036.1;
EMBL; 249880; CAA90036.1;
InterPro; IPR003597; Ig_cl.

InterPro; IPR003597; Ig_cl.

InterPro; IPR003595; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.9%; Score 52; DB 7; 52.9%; Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 1.
Pfam; PF000647; ig; 1.
ProDom; PD000328; MHC_IL_beta; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Glycoprotein; MHC II; Transmembrane.
NON TER 217 217
SEQUENCE 217 AA; 24707 MW; 1E246E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
Pfam; PF00969; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
SMART; SM00407; IGc1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of MHC class II beta chains.";
J. Immunol. 135:4095-4099(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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Gaps

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RESULT

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Q9TQA7

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bovine viral diarrhea virus strain 4998/89.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Pestivirus.
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                                                                                                                                                                                                                                                                                            Query Match 35.2%; Score 51; DB 7; Length 264; Best Local Similarity 47.1%; Pred. No. 3.9; Matches 8; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Greiser-Wilke I.M.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lower Saxony, Germany.";
Submitted (JAN 2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ302959; CAC24757.1; -.
NON TER 140 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 140
140 Aa; 15756 MW; 1A28D06B74391F74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
POPY-DRB5*0603 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.5%; Score 50; DB 12; 36.0%; Pred. No. 2.9;
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195 GEVYTCQVEHPSLPSPV 211
                                                                                                                                                                                                                                                                                                                                                                     2 GEGYQSRVDHPHFPKPI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=145184;
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NON_TER
SEQUENCE
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Q99A59;
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Q95536
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STRAIN-WISTAR FURTH;
STRAIN-WISTAR FURTH;
ATAIN-WISTAR FURTH;
Tian L., Wang M., Yu J., Kahan B.D., Stepkowski S.M.;
Than L., Wang M., Yu J., Kahan B.D., Stepkowski S.M.;
"Nuclectide sequences of three distinct complementary DNA clones encoding rat class II major histocompatibility complex RTI.D betachan proteins.";
                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99299366; PubMed-10369938;
Tian L., Wang M., Yu J., Kahan B.D., Stepkowski S.M.;
Tian L., Wang M., Yu J., Kahan B.D., Stepkowski S.M.;
Tian L., Wang M., Yu J., Kahan B.D., Stepkowski S.M.;
Than L., Wang M., Yu J., Kahan B.D., Stepkowski S.M.;
Than L., Wang M., Yu J., Kahan B.D., Stepkowski S.M.;
Invaled sequences of three distinct complementary DNA clones encoding rat class II major histocompatibility complex RT1.D betachain proteins."

Immunogenetics 49:735-737(1999).
HSSP, P13760, 2seB.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR00353; MHC_II_beta.
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; 48E220A69B374B3D CRC64;
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                                                                                                                                            01-MXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CLASS II MHC RT1.D(A) BETA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9TQA5 PRELIMINARY; PRT; 264 AA. O9TQA5.
O9TQA5.
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CLASS II MHC RTI.D(U) BETA CHAIN PRECURSOR.
RTI.D(U).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; 19; 1.
Pfam; PF00969; MHC_II_beta; 1.
SMART; SM00407; IGC1; 1.
GlyCoprotein; MHC II; Signal; Transmembrane.
SIGNAL
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                                                                                                            PRT;
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176 GEVYTCQVEHPSLPSPV 192
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192 GEVYTCQVEHPSLPSPV 208
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                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                     RT1.D(A).
Rattus norvegicus (Rat).
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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SEQUENCE
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RESULT 09TQA5

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"Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."; Immunobiology 199:105-119(1998). EMBL; AJ300675; CAC44624.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Plasmodesmal receptor, NtRPD40, mediates the trafficking of movement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                         Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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Lucas W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB 10; Length 357;
Pred. No. 7.9; 5; Indels
4; Mismatches 5; Indels
                                                                                                                                                                                                                     MEDLINE=98383416; PubMed=9717671;
Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
Leibold W., Radbruch A.;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL, AF307094; AAL09397.1; -.
                                                                                                                                                                  Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                     337 AA; 37438-MW; A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 AA; 39266 MW; 295627E59FFF3774 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB 6,
Pred. No. 7.4;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: :: :|:: |:|| | :||| 226
204 GKEFKCKVNNQALPQPIERTITK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GEGYQSRVDHPHFPKPIVRSITK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.58;
47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                            34.5%;
39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
PLASMODESMAL RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 QGFPDAVNHPNFPSTIV 338
                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 39.1.
Secondary 39.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 EGYQSRVDHPHFPKPIV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                        Equus caballus (Horse).
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                       NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0947H4;
0947H4;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins.";
                                                                                                                                                   Wagner B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
Q947H5
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                 Multiplication of Mhc-DRB5 loci in the orangutan: implications for
                   Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ρλ
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                                                                                                         SEQUENCE FROM N.A.
MEDLINE-93177102; Pubmed-8439728;
Schonbach C., Vincek V., Mayer W.E., Golubic M., O'hUigin C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laser M., Li Y., Xu L., Darden A., Wu B.X., Hazard E.S. III, Crosson C., Ma J.X.;

Crosson C., Ma J.X.;

"Identification and characterization of a novel gene induced ischemic preconditioning in the retina.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF175224; AAG09182.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50; DB 11; Length 314;
Pred. No. 6.8;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           34.5%; Score 50; DB 7; Length 142 47.1%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 142 AA; 15525 MW; 02C2C3AED44D063D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 AA; 35838 MW; 4C64B70F7E909BDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
PRECONDITIONING-INDUCIBLE GENE 1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IMMUNOGOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                  SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                  the evolution of DRB haplotypes.";
mamm. Genome 4:159-170(1993).
EMBL; S56369; AAD13881.1; -.
HSSP; P13758; 1AQD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.5%;
43.8%;
                                                                                                                                                                                                                                                                   InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GEGYQSRVDHPHFPKPI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||| :|:|| |:
73 GEGYTCQVEHPSVTSPL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 43.0-
T. Conservative
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249 NHPHLPPPLMCSVHPC 264
                                                                                                                                                                                                                                                                                                                   Lg; 1.
IGc1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                        NCBI_TaxID=9600;
POPY-DRB5*0603.
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SEQUENCE

095M34;

Q95M34 RESULT 12

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Query Match

RESULT 11 Q9ESH2 **O9ESH2**

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Klein J.

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                                                                                                                                                                                                              "Plassmodesmal receptor, NtRPD40, mediates the trafficking of movement proteins.";
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE CATIONIC AMINOACID TRANSPORTER.
Trypanosoma brucei.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                         Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A. BLORSO G.D., Paveto C.M., Flawia M.M., Torres H.N.; Pereira C.A., Alonso G.D., Paveto C.M., Flawia M.M., Torres H.N.; "Putative Trypanosoma brucei Cationic Aminoacid Transporter."; submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF250044; AAK65959.1; -SEQUENCE 539 AA; 58047 MW; El1632AE66IEC650 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                         .;
                                                                                                                                                                            Lee J.-Y., Yoo B.-C., Rojas M., Ospina N.G., Staehelin A.L.,
Lucas W.J.;
                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 10; Length 357;
Pred. No. 7.9;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.5%; Score 50; DB 5; Length 539; 42.1%; Pred. No. 12; 7; Indels ative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                               Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF307095; AAL09398.1; -.
                                                                                                                                                                                                                                                                                                    357 AA; 39276 MW; 68B7307CE83DE750 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PLASMODESMAL RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 539 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Best Local Similarity 47.1%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         3 EGYQSRVDHPHFPKPIV 19
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Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
Q965D2
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Search completed: August 26, 2002, 10:16:19 Job time: 710 sec

Service Sections Cont.

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AAY80000 standard; Peptide; 25 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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112: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
113: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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115: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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118: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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119: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
120: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
121: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
122: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
123: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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33.557 Million cell updates/sec
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                                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                    25
                                                                                                                                                                                                                                                                                                                                                                     145
1 CGEGYQSRVDHPHFPKPIVRSITKC
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Listing first 45 summaries
                                                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result			Query			
Q	Score	:	Length	BB :	ID	Description
1	145	100.0	25	21	AAY80000	Optimised IGE-CH3
7	122	84.1	(*)	21	AAY79996	Rat immunoqlobulin
3	122	84.1	340	21	AAB03643	Rat IqE heavy chai
4	122	84.1	. ,	21	AAB06206	Immunogenic peptid
2	121	83.4	45	21	AAY80018	IqE immunoqenic pe
9	121	83.4	46	21	AAY80017	IgE immunoqenic pe
7	106	73.1	25	21	AAY80001	Optimised IgE-CH3
8	105	72.4	25	21	AAY79999	Optimised IgE-CH3
6	105	72.4	45	21	AAY80019	IgE immunogenic pe
10	105	72.4	45	21	AAY80083	IqE immunoqenic pe
11	105	72.4	46	21	AAY80020	IgE immunogenic pe

logenic logenic logenic l IgE-CH human I sequence	MVF MVF MVF seque		reportue sequence o IgE immunogenic pe IgE immunogenic pe IgE immunogenic pe IgE immunogenic pe IgE-CH3 domain ant IgE immunogenic pe Iny epitope/modifi	Peptide sequence o 19E immunogenic pe Mouse immunoglobul Optimised IGE-CH3 Mouse immunoglobul Variant IGE · muta Partial canine imm Dog immunoglobuli Immunogenic peptid
AAY80081 AAY80080 AAY80084 AAY79998 AAY91212 AAY68602 AAY6014	AAY91215 AAY91216 AAY68604 AAY80007	AAY91218 AAY68605 AAY80011 AAY91213 AAY91214	AAY 80003 AAY 80016 AAY 80013 AAY 80015 AAY 80008 AAY 80012	AAY68606 AAY80078 AAY17997 AAX17415 AAX1317 AAX23317 AAX79995 AAB06208
22112211	52222	555555	5555555	21 22 21 21 21 21 21 21
7 5 6 6 6 5 7 5 6 6 6 7 5 6 6 6 7 5 6 6 6 7 6 6 6 6	44444	4 4 4 4 4 4 U R O O O A	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	63 313 25 25 110 110 312 341
72.4 72.4 71.0 71.0 71.0	71.0	71.0	71.0	711.0 665.2 611.4 58.6 57.9 56.6 56.6
105 105 103 103	103	103	103 103 103 103	10 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
12 13 14 15 10 11 18	23 23 23 23	4 2 2 2 2 4 4 2 5 5 6 6	3 3 3 3 3 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	7

ALIGNMENTS

Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglopulc; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis. Optimised IgE-CH3 domain antigen peptide for rat IgE. (UNBI-) UNITED BIOMEDICAL INC. 99WO-US13959. 98US-0100287. 15-MAY-2000 (first entry) Wang CY, Walfield AM; WPI; 2000-160578/14. W09967293-A1 21-JUN-1999; 20-JUN-1998; 29-DEC-1999 Rattus sp. Synthetic.

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy $\,\text{-}\,$

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WO200025722-A2
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22-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus sp.
                                                                                                                                                                                  Sequence
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                                              antigenic peptides (T). (T) have anti-allegic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and
                                                                                                                                                                                                                     maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylactic; anti-asthmatic; asthma; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present invention describes immunoglobulin E (IGE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE,
                                                                                                                                                                                                                                                                                                                                          Gaps
                                      present invention describes immunoglobulin E (IgE)-CH3 domain
                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                Length 25;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat immunoglobulin E epsilon heavy chain SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                             100.0%; Score 145; DB 21; 100.0%; Pred. No. 7.2e-15;
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                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 66-68; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY79996 standard; Protein; 313 AA
                                                                                                                                                                                                                                                                                                                                                                   1 CGEGYQSRVDHPHFPKPIVRSITKC 25
          Claim 1; Page 99; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunization against allergy
                                                                                                                                                                                                                                                                                                                                                                               (UNBI-) UNITED BIOMEDICAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US13959
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                                                                                                                                                                                                                                                                                                                                         25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang CY, Walfield AM;
                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-160578/14.
                                                                                                                                                                                                                                                                          25 AA;
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                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY79996;
                                                                                                                                                                                                                                                                                                                Query Match
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and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against igE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. ANY79994 to AANY80084 represent amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Pred. No. 3.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccination; infection; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat IgE heavy chain constant regions 2, 3 and 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; immunoglobulin E; IgE; vaccinatasthma; eczema; immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB03643 standard; protein; 340 AA.
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95.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0106652.
99US-0401636.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 84.1
Best Local Similarity 95.7
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 AA;
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(first entry)

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IgE immunogenic peptide conjugate SEQ ID NO:25.
15-MAY-2000
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                                                                                                                                                                                                                                                                                  Wang CY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                       ö
                                                                                                                                                                                                                                           Immunogenic peptide consisting of opossum CH2, rat CH3 and opossum CH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the rat. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.
                                                                                                                                                                                                                                                                    Rat; opossum; immunoglobulin E; IgE; vaccination; infection; allergy; asthma; eczema; immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin {\tt E} in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                         Gaps
                                       0;
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            Length 340;
                                      Indels
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3.6e-10;
            Score 122; DB 21;
Pred. No. 3.6e-10;
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Pred. No. 3.6e-1
0; Mismatches
                                       0; Mismatches
                                                                                                                                                          AAB06206 standard; protein; 341 AA
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                                                                                195 gegyqcrvdhphfpkpivrsitk 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 gegyqcrvdhphfpkpivrsitk 228
                                                                                                                                                                                                                                                                                                          Chimeric - Didelphis virginiana
Chimeric - Rattus sp.
                                                               2 GEGYOSRVDHPHFPKPIVRSITK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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           84.18;
95.78;
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Best Local Similarity 95.7%;
Matches 22; Conservative (
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                                                                                                                                                                                                                (first entry)
       Query Match
Best Local Similarity 95.7°
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 AA;
                                                                                                                                                                                                                                                                                                                                                  WO200025722-A2.
                                                                                                                                                                                                                22-NOV-2000
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                                                                                                                                                                                     AAB06206;
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                                                                                                                                               AAB06206
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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and arti-asthmatic properties. (I) induces polyglonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophis and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, eg. food allergies asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy; disease; immunisation; anti-allergic; anti-acthmatic; asthma; anaphylactic; anti-asthmatic; asthma; dermatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy {\ }^{-}
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Pred. No. 5.5e-11;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNBI-) UNITED BIOMEDICAL INC.
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Best Local Similarity 88.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Walfield AM;
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                                                                                                                                                                                                                                                                                                                                                              21-JUN-1999;
                                                                                                                                                               Unidentified
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AAY80018 standard; Peptide; 45 AA.

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RESULT AAY80018

AAY80018;

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20-JUN-1998;
                         21-JUN-1999;
 29-DEC-1999
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Synthetic.
                                                                                                Wang CY,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
AAY79999
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antibody; allergy; allergic disease; immunisation; anti-allergic;
anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                      New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy \,\text{-}\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 46;
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                                                                                                99WO-US13959.
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                                                                                                                                                                       Wang CY, Walfield AM;
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Best Local Similarity
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The present invention describes immunoglobulin E (IgE)-CH3 domain antiparatic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent anno acid sequences used in the exemplification of the present invention.
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80.0%; Pred. No. 5.2e-09;
iive 0; Mismatches 5;
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98US-0100287.
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Best Local Similarity 80.0
Matches 20; Conservative
                                                                                                                                                        Walfield AM;
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for immunization against allergy

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antigence therefore the control of the control of the present and anti-anaphylactic and anti-ashmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, and downregulation of IgE synthesis. Conjugates, or fusion peptides, allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for combinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             maximize cross reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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                                                                                                          New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy \,^{\text{-}}
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ilarity 76.0%; Pred. No. 7.3e-09;
Conservative 0; Mismatches 6;
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("NBI-) UNITED BIOMEDICAL INC
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                                    Claim 14; Page 76; 155pp; English.
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antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and sownregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope. (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention.
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                (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                            Indels
Conjugates of (I) that include a promiscuous T helper
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                                                                                                                                                                                                                     Score 105; DB 21;
Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IgE immunogenic peptide conjugate SEQ ID NO:88.
                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                  72.4%;
76.0%;
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                             46 AA;
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                                                    72.4%; Score 105; DB 21; Length 57; 76.0%; Pred. No. 1.8e-08; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                               IgE immunogenic peptide conjugate SEQ ID NO:87.
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                                                                                                                           1 CGEGYQSRVDHPHFPKPIVRSITKC 25
                                                                                                                                            Claim 14; Page 77; 155pp; English
                                                                                                                                                                                                                                                   AAY80080 standard; Peptide; 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNBI-) UNITED BIOMEDICAL INC
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                                                                     Local Similarity 76.0
tes 19; Conservative
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 57
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunosenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergic disease; immunisation; anti-allergic; anti-anti-antitic; asthma:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for immunization against allergy
1 CGEGYQSRVDHPHFPKPIVRSITKC
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Score 105; DB 21; Length 62; Pred. No. 2e-08; 0; Mismatches 6; Indels

72.4%; 76.0%;

Query Match 72.4 Best Local Similarity 76.0 Matches 19; Conservative

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The present invention describes immunoglobulin E (1gE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                 Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; antiallergic; anti-ashmatic; asthma; anaphylactic; anti-ashmatic; asthma; anaphylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy ^{\rm -}
                                                                                                                                          Optimised IgE-CH3 domain antigen peptide for human IgE.
                 AAY79998 standard; Peptide; 25 AA.
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AAY79998
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Gaps ; 0 Length 25; 5; Indels Score 103; DB 21; Pred. No. 1.5e-08; 3; Mismatches 5; 71.0%; 68.0%; 17; Conservative Query Match Best Local Similarity Matches

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1 CGEGYQSRVDHPHFPKPIVRSITKC 25

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68.0%; Pred. No. 1.7e-09;
Live 3; Mismatches 5;
                        5455030-1

US-08-890-719-12

US-08-890-719-13

US-08-890-719-13

US-08-890-719-13

US-08-890-719-13

US-08-835-400-8

US-08-579-940-7

US-08-579-940-7

US-08-579-940-7

US-08-578-469-18

US-08-765-469-18

US-08-630-172-20

US-08-630-172-20

US-08-630-172-19

US-08-630-172-19

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US-08-630-172-19

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US-08-630-172-19
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20.JUNE-1998
CLASSIFICATION: 4.24
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELEPHONE: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
"WUTER: IBM PC COMPATIBLE
"VETEM: PC WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGEGYQSRVDHPHFPKPIVRSITKC 25
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 68.0 Matches 17; Conservative
; MOLECULE TYPE: peptide US-09-100-4148-95
336.6
   \begin{smallmatrix} 5533 \\ 4444 \\ 4469 \\ 888 \\ 8444 \\ 445 \\ 888 \\ 8444 \\ 445 \\ 888 \\ 844 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445 \\ 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 95, Al Sequence 99, Al Sequence 99, Al Sequence 99, Al Sequence 99, Al Sequence 101, Sequence 97, Al 
                                                                                                                                                                                                   August 26, 2002, 10:05:18; Search time 34.18 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-303-323-95
US-09-100-414B-98
US-09-100-414B-99
US-09-303-323-98
US-09-303-323-99
US-09-303-323-99
US-09-303-323-100
US-09-100-414B-101
US-09-100-414B-96
US-09-100-414B-97
US-09-100-414B-97
US-09-100-414B-97
US-09-100-414B-102
US-09-303-323-97
US-09-303-323-97
US-09-303-323-97
US-09-303-323-97
US-09-303-323-97
US-08-335-583-2
US-08-335-584-2
US-08-332-5399-54
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1 CGEGYQSRVDHPHFPKPIVRSITKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231628 seqs, 24425594 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                       US-09-701-623C-7
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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                                                                                                                                                                                                         Run on:
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 103; DB 3; Length 42; Pred. No. 3e-09;
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Sequence 99, Application US/09100414B
Sequence 99, Application US/09100414B
Sequence 99, Application US/09100414B
Sequence 99, Application US/09100414B
Sequence 99, Application US/0910041B
Sequence 99, Application US/0910041B
Sequence 99, Application US/0910041B
Sequence 99, Application US/0910041B
Sequence 99, Application US/091041B

SOFTWARE: WORD 9/
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MATAH L.Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-754-6849
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: maino acids
TYPE: maino acids
TYPE: MINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1151-4157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 CGETYQSRVTHPHLPRALMRSTTKC 42
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NAME: MATIA H. LID
RECISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPHONE: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09,
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.0%;
68.0%;
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INFORMATION FOR SEQ ID NO: 99
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 68.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-98
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ZIP: 10154-0054
COMPUTER READABLE FORM:
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US-09-100-414B-99
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STATE:
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Best Local Similarity 68.0%; Pred. No. 1.7e-09;
Matches 17; Conservative 3; Mismatches 5; Indels
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Sequence 98 Application US/09100414B
Fatent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: INWINGENS
TITLE OF INVENTION: INWINGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                     Sequence 95, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZIP: 10154-0054

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97

CURRENT APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFRAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGEGYQSRVDHPHFPKPIVRSITKC 25
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CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 95: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-09-303-323-95
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                                                                                                                                                                                                                                                                                                                                                                                                    New York
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                                    US-09-303-323-95
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STATE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 99, Application US/09303323
Fatent No. 6228987
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                 FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INPORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECHONE: 212-758-4800
TELECHONE: 212-758-4800
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGEGYQSRVDHPHFPKPIVRSITKC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.08;
                                                                                                                                                                                                                                                                                                                                                                                                                        42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.0 Best Local Similarity 68.0 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-09-303-323-98
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 42 ammunone: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-09-303-323-99
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Pred. No. 3e-09;
3; Mismatches 5; Indels
                         Indels
                       5;
                       Mismatches
                                                                                                                                                                                                                                         APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNGENS
TITLE OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFRENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 98, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: IMMUNOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                      Sequence 100, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               STA'E.
COWTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~AMPUTER: IBM PC compatible
                                                                              18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                         1 CGEGYQSRVDHPHFPKPIVRSITKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 GGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CGEGYQSRVDHPHFPKPIVRSITKC 25
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68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word 97
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 17; Conservative
                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10154-0054
                                                                                                                                                                     US-09-100-414B-100
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                 17;
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US-09-303-323-98
Matches
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Length 45;
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Pred. No. 3.2e-09;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL LHRH PEPTIDE TITLE OF INVENTION: NOVEL LHRH PEPTIDE TITLE OF INVENTION: INMUNOGENS NUMBER OF SEQUENCES: 106 CORRESPONDENCE ADDRESS: ADDRESSE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: C. T.L.C....
SOFTWARE: WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20.JUNE-1998
CLASSIFICATION: 4.24
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
RAGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEFAN: 212-754-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 antho acids
TUBER AND ACIDS
TOTAL CONTROL OF THE CONTROL OF 
                                 GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
                                                                                                                                                                                                                 ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOGTWARE: MOCK 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30.APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 101, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 CGETYQSRVTHPHLPRALMRSTTKC 45
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                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
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68.0%;
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                                                                                                                                                          NUMBER OF SEQUENCES: 1(CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
            Patent No. 6025468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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Pred. No. 3e-09;
3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 100, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY AGENT INFORMATION:
NAME: Maria H. Lin
REGISTATION NUMBER: 29,323
REFERENCE/DOCKET 1151-4157
TELECOMMUNICATION INFORMATION:
TELEFRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue
CIIY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC Windows SOFTWARE: Word 97 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/303,323 FILING DATE: 30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT', 9
US-09-100-414B-101
; Sequence 101, Application US/09100414B
                                                                                                                                                                                                                                                                                                                                                                   1 CGEGYQSRVDHPHFPKPIVRSITKC 25
                                                                                                                                                                                                                                                                                                                                                                                              1 CGEGYQSRVDHPHFPKPIVRSITKC 25
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                                                                                                                                                                                                                                               71.0%;
68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 68.09
Matches 17; Conservative
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                                                                                                                         ; MOLECULE TYPE: peptide US-09-303-323-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-303-323-100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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22 CGETYQSRVTHPHLPRALMRSTTKC 46
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 46 amino acids
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                              US-09-100-414B-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-100-414B-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.0%; Score 103; DB 4; Lv 68.0%; Pred. No. 3.2e-09; Live 3; Mismatches 5;
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                                                                                                                         REGISTRATION NUMBER: 29,323
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFRAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1151-4157
                             ÅPPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGEGYQSRVDHPHFPKPIVRSITKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 CGETYQSRVTHPHLPRALMRSTTKC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT IRPORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.09
Best Local Similarity 68.09
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    : 45 amino acids amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-09-303-323-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                     OPERATION SYSTEM: PC WINDOWS
SOFTWARE: WORD 97
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 20-JUNE-1998
CLASSIFTCATION: 424
ATTONNEY, AGENT INFORMATION:
NAME: MAINE: H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/POCKET NUMBER: 1151-4157
TELECOMMUNICATION:
TELEPHONE: 212-751-6849
                                        GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TILLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
Sequence 97, Application US/09100414B Patent No. 6025468
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; Sequence 96, Application US/09303323
; Patent No. 6228987
                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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Gaps
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                                                                                                                                                                                     Length 46;
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                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                              Score 103; DB 4; L
Pred. No. 3.3e-09;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 102, Application US/09100414B
Fatent No. 6023468
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: NOVEL CANNOTED
CORRESPONDENCE ADDRESS:
ADDRESSE: 
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OUPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/POCKET VUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPHONE: 212-758-4800
TELEPHONE: 212-751-6849
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 aniho acids
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                                                                                                                                                                                                                                                                                                                    1 CGEGYQSRVDHPHFPKPIVRSITKC 25
                                                                                                                                                                                                                                                                                                                                                          22 CGETYQSRVTHPHLPRALMRSTTKC 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                     71.0%;
68.0%;
                                                                                                                                                                              Query Match
Best Local Similarity 68.0°
Matches 17; Conservative
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Best Local Similarity 68.0%
Matches 17; Conservative
                                               ; MOLECULE TYPE: peptide US-09-303-323-97
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MOLECULE TYPE: peptide
                    TOPOLOGY: linear
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Pred. No. 3.3e-09;
3; Mismatches 5; Indels
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Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: NOVEL CANNOTEDE
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTGAR & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
OF ILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758 4800
INFORMATION FOR SEQ. ID NO: 96:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFFCATION:
PROR APPLICATION UNBER: 09/100,414
FILING DATE: 20-UNE-1998
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION:
TELEPHONE: 212-758-4800
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 68.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE; amino acid
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TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-09-303-323-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model
Run on:
August 26, 2002, 10:04:25; Search time 45.87 Seconds
(without alignments)
52.370 Million cell updates/sec
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Title: US-09-701-623C-8 Perfect score: 140

Sequence: 1 CGYGYQSIVDRPDFPKPIVRSITLC Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 08

Maximum Match 100% Listing first 45 summaries

Database: PIR_71:*

1: pirl:

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ig epsilon chain C IgE chain C3 regio IgE chain C3 regio Ig epsilon chain C Ig epsilon chain C Ig epsilon chain C Mypothetical prote conserved hypothet MAK32 protein - ye cytochrome-c oxida phosphate butyrylt pitrilysin (EC 3.4 cytochrome-c oxida probable porphobil probable acetolact NADH dehydrogenase adenine phosphorib probable enoyl-CoA NADH dehydrogenase hypothetical prote adenine phosphorib cycle protein nypothetical prote probable fadĒ36 pr probable phosphori protein K04A8.1 [i Ig epsilon-chain cell cycle protei Description SUMMARIES EHMS S38864 EHRT S12142 G72293 T06521 A35209 E71532 B95963 AD0311 C75399 EHMSS 168730 168726 AG2525 C75354 A75026 BVBYK2 AG0531 S72706 G91024 F31043 136948 B70801 A71211 554628 ID Query Match Length DB 429 1165 232 232 4033 363 1169 1169 2114 2110 3114 359 Score 49 48.5 48 1116 1108 1108 1108 108 45 49 49 Result No.

281 GYGYQCVVDRPDFPKPIVRSITL 303

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Lucious Chain C3 region - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C; Accession: 168730
R; Shinkai, Y; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A; Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic aci
A; Reference number: 154443; MUID: 88152907

A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: mRNA A.Residues: 1-107 <RES> A.Cross-references: GB:M22933; NID:g194464; PIDN:AAA37915.1; PID:g194469

NADH dehydrogenase NADH dehydrogenase	NADH dehydrogenase	transcription fact	statherin precurso	beta-amylase (EC 3	phosphoesterase-re	hypothetical prote	probable membrane	pol protein - simi	cytochrome-c oxida	translation initia	L-ascorbate oxidas	probable DNA repli	elongation factor	P-type ATPase - sl
A65000 H85868	AI0796	G02326	SBHUP	838779	A87198	T16904	S55151	D49281	OLBO4	T39767	KSKVAO	B72775	D83112	T30580
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32.1 9							_							31.4
			31.8		31.8		_							44 31.4

ALIGNMENTS

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RESOLT 1
EMENSITY 1
EMENSITY 1
EMENSITY 1
EMENSITY 1
INTERIOR Credion (version 2) - mouse

C.Species: Mus musculus (house mouse)
C.Species: 30-Jun-1987 was quence_revision 30-Jun-1987 text_change 16-Aug-1996
C.Date: 30-Jun-1987 wasquence_revision 30-Jun-1987 text_change 16-Aug-1996
C.Date: 30-Jun-1987 wasquence_revision 30-Jun-1987 text_change 16-Aug-1996
C.Date: 30-Jun-1987 wasquence_revision 30-Jun-1987 text_change 16-Aug-1996
R.Ishida, N. 1017-1123, 1982
R.Ishida, N. 117-1123, 1982
A.Jun-1987 wasquence of the mouse immunoglobulin epsilon gene: comparison A; Reference number: A09066; MUID: 84236092
A.Jun-1987 was determined from the germline gene
A.Jun-1987 was determined from the germline gene
C.Genetics:
A.Jun-1987 was determined from the genetics
C.Genetics:
A.Jun-1987 was determined from the germline genetics
C.Genetics:
A.Jun-1987 was determined from the germline genetics
C.Genetics:
A.Jun-1987 was determined from the genetics
C.Genetics:
A.Jun-1987 was determined from the genetics
C.Gen
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us-09-701-623c-8.open.rpr

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Gaps

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Indels

Length 548;

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A; Molecule type: mRNA
A; Residues: 1-429 <HELD-
A; Residues: 1-429 <HELD-
A; Experimental source: Strain LOU/c/Wsl, immunocytoma IR2
B; Kindsvogel, W. R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
DNA 1, 335-343, 1982
A; Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction
A; Reference number: A90937; MUID:83182019
A; Contents: myeloma IR162
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F;223-291/Domain: immunoglobulin homology <IM3>
F;327-398/Domain: immunoglobulin homology <IM4>
F;37-398/Domain: immunoglobulin homology <IM4>
F;46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predi
                                                                                                                                                                                                                                                                 C; Accession: S38664
R; Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A; Reference number: S38664
A; Recession: S38664
A; Status: preliminary
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-548
A; Cross-references: EMBL: 227397; NID: 9416537; PIDN: CAA81788.1; PID: 9940782
C; Superfamily: immunoglobulin C region; immunoglobulin homology
F; 353-421/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accession: A93442; A90937; A02143
R;Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A;Title: Structure and evolution of the heavy chain from rat immunoglobulin
A;Reference number: A93442; MUID:83064537
                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 06-Jan 1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 429;
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77.3%; Pred. No. 4.2e-05;
Live 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.1%; Score 108; DB 2; L 90.9%; Pred. No. 1.6e-08; Live 0; Mismatches 2;
                                                                                                                                                              Ig epsilon chain C region - mouse (fragment)
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ses 17; Conservative
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Matches 20; Conserv
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Matches
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F:1-44.Domain: immunoglobulin homology (fragment) <IMI>F;B1-64.Domain: immunoglobulin homology <IM2>F;B1-6254.Domain: immunoglobulin homology <IM3>F;290-361/Domain: immunoglobulin homology <IM3>F;290-361/Domain: immunoglobulin homology <IM4>F;10,51,62,133,205,228,332,8B2/Binding site: carbohydrate (Asn) (covalent) #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     igE chain C3 region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O2-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: 168726
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid A;Reference number: 154443; MulD:88152907
A;Accession: 168726
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A02144
R;Liu, F:T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
A;Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.
A;Reference number: A02144; MUID:83117774
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
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C;Superfamily: immunoglobulin C region; immunoglobulin homology F;22-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                     Score 108; DB 2; L. Pred. No. 2.6e-09; 0; Mismatches 2;
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Pred. No. 2.6e-09;
O; Mismatches 2;
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Pred. No. 1.1e-08;
0; Mismatches 2;
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Best Local Similarity 90.9%;
Matches 20; Conservative
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90.98;
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Best Local Similarity 90.9
Matches 20; Conservative
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Mosines: 1-433 <MHI>
A;Cross-references: 1-433 <MHI>
A;Experimental source: strain Rl
C;Genetics:
A;Gene: DR1773
A;Map position: 1
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A; Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50647.1; PID:g545
A; Experimental source: strain Orsay
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A; Title: The PET18 locus of Saccharomyces cerevisiae: a complex locus containing mult A; Reference number: S07692; MUID:89131254
A; Accession: S07695
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A, Accession: A75026
A; Status: preliminary
A; Molecule type: DNA
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C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1991 #sequence_revision 30-Sep-1993 #text_change 16-Jun-2000
C;Accession: S19429; S0769;
R;Feldmann, H.; Mannhaupt, G.; Vetter, I.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19429
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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C;Superfamily: phosphoribosylformylglycinamidine synthase component
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A; Residues: 1-14,'I',15-81,83-282,'S',284-363 <TOH>
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Pred. No. 14;
7; Mismatches
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A;Gene: SGD:MAK32; MIPS:YCR019w
A;Cross-references: SGD:S0000612; MIPS:YCR019w
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R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
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513 YNEVVDRPVKPTPVVAGI 530
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Best Local Similarity 35.3
Matches 6; Conservative
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Matches 9; Conserv
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A; Molecule type: DNA
A; Residues: 1-363 <FEL>
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hypothetical protein alr7383 [imported] - Anabaena sp. (strain PCC 7120) plasmid pCC7126
C;Species: Anabaena sp.
A;Note: Anabaena sp.
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C;Accession: AG2525
C;Accession: AG2525
NARaeko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi NARazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; WUID:21595285; PMID:11759840
A;Status: preliminary
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R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
Science 286, 1571-1577, 1999

A. Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A; Reference number: A75250; MUID: 20036896
                                                                                                                                                                                                                                                      an
                                                             C; Species: Sulfolobus sp.
C; Accession: T31043
R; She, O.; Phan, H; Garrett, R.A.; Albers, S.V.; Stedman, K.M.; Zillig, W.
Extremophiles 2, 417-425, 1998
A; Title: Genetic profile of pNOB8 from Sulfolobus: the first conjugative plasmid from A; Reference number: 220959; MUID:99044580
A; Reference number: 220959; MUID:99044580
A; Reference number: Zillig; MuiD:99044580
A; Residue; Preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-165 <SHE>
A; Residues: 1-165 <SHE>
A; Conservation of the conser
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A; Residues: 1-232 <KUR>
A; Cross-references: GB:BA000020; PIDN:BAB77141.1; PID:g17134582; GSPDB:GN00180
A; Experimental source: strain PCC 7120
C; Genetics:
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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Pred. No. 4.9;
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7.2;
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T31043 * hypothetical protein 165 - Sulfolobus sp. plasmid pNOB8
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Pred. No. 7.2;
5; Mismatches
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Best Local Similarity 58.8%;
Matches 10; Conservative ;
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43.8%;
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Best Local Similarity 43.0.
The Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Cross-references: GB: J05425; NID: g203516; PIDN: AAA40949.1; PID: g203517
A; Cross-references: GB: J05425; J990
A; A; Muclei Acida Res. 18, 3992, 1990
A; Tille: Complete nucleotide sequence of the gene encoding rat cytochrome c oxidase s A; Reference number: S12724; MuID: 90326528
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 11-Jun-1999
C;Accession: A35209; S12724; S004700; S04593; S14190; S65373
R;Yamada, M : Anuro, N : Goto, Y : Okazaki, T .
J. Biol. Chem. 265, 7687-7692, 1990
A;Title: Structural organization of the rat cytochrome c oxidase subunit IV gene.
A;Reference number: A35209; MUID:90237079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Pissum sativum (garden per C:Species: Il-Jun-1999 #sequence_revision Il-Jun-1999 #text_change 21-Jul-2000 C:Date: Il-Jun-1999 #sequence_revision Il-Jun-1999 #sequence_revision In-Jun-1999 #sequence_revision In-Jun-1999 #sequence_revision In-Jun-1999 #sequence_revision In-Jun-1999 #sequence_revision In-Jun-1999 #text_change 21-Jul-2000 R:Vancession In-Jun-1999 #sequence_revision In-Jun-1999 #sequence 
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A;Status: preliminary
A;Status: DNA
A;Residues: 1-169 <AMU>
A;Residues: 1-169 <AMU>
A;Cross-references: EMBL:J05425; NID:g203516; PIDN:AAA40949.1; PID:g203517
B;Goto, Y; Amuro, N; Okazaki, T.
Nucleic Acids Res. 17, 2851, 1989
A;Title: Nucleotide sequence of cDNA for rat brain and liver cytochrome c A;Reference number: S04070; MUID:89240039
A;Accession: S04070
A;Accession: S04070
A;Molecule type: mRNA
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                                                                                                    Length 294;
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Pred. No. 68;
5; Mismatches
                                                                                                    ; DB
                                                                                                                                                                         6; Mismatches
                                                                                                    Score 48;
Pred. No.
C; Superfamily: phosphate acetyltransferase
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Best Local Similarity 38.1%;
Matches 8; Conservative
                                                                                                    34.38;
                                                                                                                                 Best Local Similarity 46.7 Matches 7; Conservative
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122 SVMEIPDFPRPLIIS 136
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C;Reywords: membrane-associated complex; mitochondrion; oxidative phosphorylation; oxidd
F;1-22,Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;23-169/Product: cytochrome-c oxidase chain IV #status predicted <MAT>
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on, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-&eferences: GB:AE001770; GB:AE000512; NID:g4981658; PIDN:AAD36206.1; PID:g498167
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sec
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C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C; Accession: G72293
R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 399, 323-329, 1999
A;Title: B'idence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316
A;Accession: G72293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytochrome-c oxidase (EC 1.9.3.1) chain IV precursor - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: Si2142; SiGl14
R; Grossman, L.I.; Akamatsu, M. Nucleic Acids Res. 18, 6454, 1990
A; Title: Nucleotide sequence of a mouse cDNA for subunit IV of cytochrome c A; Reference number: S12142; MUID:91057158
                                                                                                                                                                                                             Gaps
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A; Residues: 1-169 <GRO>
A; Cross-references: EMBL:X54691; NID:950518; PIDN:CAA38507.1; PID:950519
A; Experimental source: strain Balb/c
R; Carter, R.S.; Avadhani, N.G.
Arch. Biochem. Biophys. 288, 97-106, 1991
A; Title: Cloning and characterization of the mouse cytochrome c oxidase s
A; Reference number: S16114; MUID:91378465
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Pred. No. 7.2;
5; Mismatches 9; Indels
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61 GLKWIVDRGSDFPKEVIREI 80
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ilarity 36.4%;
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                                                                                                                                     Query Match 34.6
Best Local Similarity 55.0
Matches 11; Conservative
A; Map position: 3R
C; Superfamily: MAK32 protein
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es 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-294 <ARN>
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A;Residues: 1-169 <ARC>
C;Genetics:
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RiGopalan, G.; Droste, M.; Kadenbach, B.
Nucleic Acids Res. 17, 4376, 1989
A:Title: Nucleotide sequence of cDNA encoding subunit IV of cytochrome c oxidase from fe
A;Reference number: S04593; MUID:89296488
A;Accession: S04593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A: Description: the cytochrome-c oxidase complex catalyzes the oxidation of four molecule in from the mitochondrial matrix producing two molecules of water and lowering the conces, standard or construction of the mitochondrial matrix producing two molecules of water and lowering the conces. Superfamily: cytochrome-c oxidase chain IV
F:1-22/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:23-169/Product: cytochrome-c oxidase chain IV #status predicted <TNP>
F:73-103/Domain: transmembrane helix #status predicted <TR01>
                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X15029; NID:955980; PIDN:CAA33133.1; PID:955981
R;Virbasius, J.V.; Scarpulla, R.C.
Nucleic Acids Res. 18, 6581-6586, 1990
A;Title: The rat cytochrome c oxidase subunit IV gene family: tissue-specific and hormon A;Reference number: S14190; MUID:91067442
A;Accession: S14190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A) Experimental source: strain Sprague Dawley
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1990
B:Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Bur. J. Blochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
A;Reference number: $65372; MUID:95324529
A;Accession: $65373
                                                                   Cross-references: EMBL:X14209; NID:g55989; PIDN:CAA32426.1; PID:g55990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: X54081; NID: 957030; PIDN: CAA38018.1; PID: 957031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-169 <VIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 25/1; 81/1; 125/1
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                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-169 <GOP>
A; Residues: 1-169 <GOT>
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Search completed: August 26, 2002, 10:04:25 Job time: 71 sec

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Gaps

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10; Indels

Mismatches

2;

Query Match
Best Local Similarity 45.5'
Matches 10; Conservative

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33.6%; Score 47; DB 1; Length 169; 45.5%; Pred. No. 10;

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Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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              saimiri sci
bacteriopha
                                     bacteriopha
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                                                                                                  homo sapien
gallus gall
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                                                                                                                           homo sapien
 saimiri
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MEDIINE=84236092; Pubmed=6329728;
Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison with the human epsilon gene sequence.";
EMBO J. 1:1117-1123(1982).
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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## PIR; A02144; EHMS.

## RSPP, POR1854; IEHMS.

## RSPP, POR1854; IEHMS.

## RSPP, POR1854; IIGE.

## InterPro; IPR003606; Ig_MHC.

## InterPro; IPR003597; Ig_cl.

## InterPro; IPR003509; Ig_like.

## SMART; SM00410; Ig_like; 2.

## SMART; SM00407; Ig_like; 2.

## RSMART; SM00407; Ig_like; 3.

## RPOSITE; PS00290; Ig_MHC; 3.

## Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.

## NOW_TER 1 90 CH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECURINCE OF 34-421 FROM N.A. MEDLINE-83117774; PubMed-6818553; Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.; "Cloning and nucleotide sequence of mouse immunoglobulin epsilon
          046582
P08765
038039
P03633 1
P03633 1
P01854 1
P090854 1
P4854 1
P35562 m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
                                                                                                                                                                                                                                      EPC_MOUSE STANDARD; PRT; 421 AA. 196336; P01856; Call Tuly-1986 (Rel. 31, Last sequence update) 15-UUL-1999 (Rel. 33, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update) Mus musculus (Mouse).
                                                                                                                                                                           ALIGNMENTS
           COX4_SAISC
VGD_BPAL3
VGD_BPPHK
VGD_BPG4
APT_PSEAE
YGT5_YEAST
EPC_HUMAN
IRK3_CHICK
IRK3_CHICK
                                                                                                                                       FRK3_MOUSE
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CH2
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 DOMAIN
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P23066 saccharomyc

94658 pyrhecia pi

P19783 mus musculu

99x014 thermotoga

P1088 rattus norv

084301 chlamydia t

025578 lyrechinus

059521 pyrococcus

P7335 synechocyst

P53356 mycobacteri

P3300 salmonella

P3300 salmonella

P3300 salmonella

P3300 salmonella

P3390 salmonella

P3391 saccharomyc

04689 cebus apell

P6884 cottaromyc

04689 cebus apell

04686 perodicticu

04689 cebus apell

04689 cebus apell

04689 cetus azara

P00423 bos taurus

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P14133 cucumis sat

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                                                                                    August 26, 2002, 10:17:03; Search time 24.08 Seconds
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                          1 CGYGYQSIVDRPDFPKPIVRSITLC 25
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COX4_CEBAP
COX4_PERPO
COX4_AOTAZ
COX4_BOVIN
COX4_BOVIN
IF34_SCHPO
ASO_CUCSA
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KPC1_LYTPI
PURL_PYRHO
APT_SYNY3
ECHC_MYCLE
NUOG_ECOLI
NUOG_SALTY
NFC2_HUMAN
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AMYB_SECCE
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DSC1_MOUSE
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PURL_PYRAB
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PTA_THEMA
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COX4_PITPI
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InterPro; IPR003597; Ig_cl
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Heilig R.;
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Q9UXW6;
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0
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.; "Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hellman L., Pettersson U., Bennich H.; "Characterization and molecular cloning of the mRNA for the heavy (epsilon) chain of rat immunoglobulin E."; Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
MEDLINE-83182019; PubMed-6820340;
Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
construction, identification, and DNA sequence.";
DNA 1:335-343(1982).
                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                               Length 421;
                                                                                                                                                                                              Score 108; DB 1; Length 42
Pred. No. 6.9e-09;
); Mismatches 2; Indels
                                                                                                                                                              8F909E1F30A06B47 CRC64;
          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (
                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
gesilon chain C region.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                         429 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 10:6041-6049(1982)
                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MBL; J00744; AAA41379.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-LOU/C/WSL;
MEDLINE-83064537; Pubmed-6292865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 205-306 FROM N.A. MEDLINE-82174576; PubMed-6803238;
                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                        280 GYGYQCIVDHPDFPKFIVRSIT 301
                                                                                                                                                                                                                                           2 GYGYQSIVDRPDFPKPIVRSIT 23
                                                                                                                                                              47320 MW;
                                                                                                                                                                                              77.1%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                    20; Conservative
                                                                                                                                                                                                                                                                                                                         STANDARD;
  421
75
180
285
392
43
72
84
84
95
166
238
261
365
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43
72
166
238
261
365
415
421 AA;
                                                                                                                                                                                                           Similarity
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HSSP; P01854; 1IGE.
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
DOMAIN
DISULFID
DISULFID
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CARBOHYD
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CARBOHYD
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CARBOHYD
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                                                                                                                                                 CARBOHYD
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Best Local 8
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EPC_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Buryārchaeota; Thermococcales; Thermococcaceae; Pyrococcus NCBL_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phosphoribosylformylglycinamidine synthase II (EC 6.3.5.3) (FGAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.0%; Score 49; DB 1; Length 705; 50.0%; Pred. No. 11:
                                                                                                                                                                                                                                                           Length 429
                                                                                                                                                                                                                                       Score 85; DB 1; Length 422
Pred. No. 2.2e-05;
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                                                                                                                                                   R -> N (IN REF. 2).
P -> L (IN REF. 2).
; D2970B34EF8A72B0 CRC64;
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8D75A4AEEB102499 CRC64;
                                                                                 PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin domain; Immunoglobulin C region.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 705 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO00728; AIRS_related. Pfam; PF00586; AIRS; 2. Pfam; PF02769; AIRS_C; 2.
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                                                                                                                                                                                                                                                                                                                                                                       284 GEGYQCRVDHPHFPKPIVRSIT 305
                                                                                                                                                                                                                                                                                                                                             2 GYGYQSIVDRPDFPKPIVRSIT 23
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                                                                                                                                                                                             48671 MW;
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SEQUENCE 705 AA; 77866 MW;
IPR003600; Ig_like.
                                                                                                                                                                                                                                                           60.7%;
77.3%;
                 Pfam; PF00047; ig; 4. SMART; SMO0410; IG_like; 3. SMART; SMO0407; IGcl; 1.
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                                                                                                                                                                                                                                                           Query Match 60.7
Best Local Similarity 77.3
Matches 17; Conservative
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Best Local Similarity 50.0°
Matches 9; Conservative
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308
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429 AA;
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Mus musculus (Mouse)
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                                                                                                                                   c + 2 H(2)0
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P19783;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                               Feldmann H., Mannhaupt G., Vetter I.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NECESSARY FOR THE STRUCTURAL STABILITY OF L-A DOUBLE-
STRANDED RNA-CONTAINING PARTICLES. NECESSARY FOR GROWTH AT 37
DEGREES CELSIUS AS WELL AS FOR MAINTENANCE OF THE KILLER PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Pitheclinae;
                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                MEDLINE-89131254; PubMed-3916862;
Toh-E A., Sahashi Y.;
"The PET18 locus of Saccharomyces cerevisiae: a complex locus
containing multiple genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.6%; Score 48.5; DB 1; Length 363; 55.0%; Pred. No. 6.2; ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Cytochrome c oxidase polypeptide IV (EC 1.9.3.1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I -> II (IN REF. 1).
MISSING (IN REF. 1).
CFB358F8ACF6EA4C CRC64;
                                                                                                01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                363 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 AA
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                                                              PRT;
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                                                                                   (Rel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40783 MW;
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PIR; S19429; BVBYK2.
SGD; S0000612; MAK32.
InterPro; IPR00213; PfkB.
Pfam; PF00294; pfkB; 1.
Pfam; PF00294; pfkB; 1.
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513 YNEVVDRPVKPTPVVAGI 530
                                                                                                                                MAK32 OR YCR019W OR YCR19W.
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61 GLKWIVDRGSDFPKEVIREI
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Best Local Similarity 55.0
Matches 11; Conservative
                                                              STANDARD;
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                                                                                                                                                                                                                                                              /east 1:159-171(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 AA;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                       protein.
                                                                                    01-NOV-1991
                                                                                               01-MAY-1992
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O46585;
                                                             MK32_YEAST
P23060:
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                                       MK32_YEAST
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                                                                                                                                                                                                                                                    MITOCHONDRIAL ELECTRON TRANSPORT.
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SEQUENCE FROM N.A.
MEDLINE=97277139; PubMed=9115172;
MU W., Goodman M., Lomax M.I., Grossman L.I.;
Mulecular evolution of cytcchrome c oxidase subunit IV: evidence for positive selection in simian primates.";
J. Mol. Evol. 44.477-491(1997).
-!- FUNCTION: THIS PROPEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTCCHROME C OXIDASE, THE TERMINAL OXIDASE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter R.S., Avadhani N.G.;
"Cloning and characterization of the mouse cytochrome c oxidase
"Loning and characterization of the mouse cytochrome c oxidase
subunit IV gene.";
Parch. Biochem. Biophys. 288:97-106(1991).
-!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytochrome c oxidase polypeptide IV, mitochondrial precursor
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Pred. No. 2.8;
2; Mismatches
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Last annotation update)
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EMBL; AF042768; AAB97849.1; JOINED.
EMBL; AF042769; AAB97849.1; JOINED.
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MEDLINE=91057158; PubMed=2173832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91378465; PubMed=1654830;
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01-0CT-1993 (Rel. 27, Last seq
16-0CT-2001 (Rel. 40, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; Mitochondrion.
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.vv,
-Local 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004203; COX4. 
Pfam; PF02936; COX4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 YGYQSIVDRPDFPKPIVRSI
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EC 1.9.3.1).
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P10888;
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-MASB / DSM 3109;
STRAIN-MASB / DSM 3109;
MEDLINE-99287316; Pubmed-10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
Mature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                               MO -> IE (IN REF. 1; AAB02139 AND IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE OF 1-39, AND CHARACTERIZATION.

BELLINE-29173910; PubMed-10074080.

BOCK A.-K., Glasemacher J., Schmidt R., Schoenheit P.;

Purification and characterization of two extremely thermostable endrymes, phosphate acetyltransferase and acetate kinase, from the hyperthermophilic eubacterium Thermotoga maritima.";

J. Bacteriol. 181:1861-1867(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phosphate acetyltransferase (EC 2.3.1.8) (Phosphotransacetylase).
                                                                                                                                                                                                                                                                 MITOCHONDRION.
CYTOCHROME C OXIDASE POLYPEPTIDE IV.
A -> R (IN REF. 1).
S -> N (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 1; Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
                                                                                                                                                                                                                                                                                                                                       D30B1DBBE14FDBEA CRC64;
                                                                                                                                                                                                                                                      Oxidoreductase; Mitochondrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 AA.
                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Thermotogales; Thermotoga.
NCBL_TaxID=2336;
                                                                                                                  EMBL; M37831; AAB02139.1; -.
EMBL; M58034; AAB02139.1; JOINED.
EMBL; M37829; AAB02140.1; -.
EMBL; X54691; CA338507.1; -.
PIR; S12142; S12142.
PIR; S12508; S12508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                         3 YGYQSIVDRPDFPKPIVRSITL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                       33 YAFPTYADRRDYPLPDVAHVTM 54
                                                                                                                                                                                                                                                                                                                                       169 AA; 19530 MW;
                                                                                                                                                                                                                                                                                                                                                                         34.38;
36.48;
                                                                                                                                                                                                     HSSP; P00423; 10CC.
MGD; MGI:88473; Cox4.
InterPro; IPR004203; COx4.
Pfam; PF02936; COx4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 8; Conserv
c + 2 H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTA OR TM1130
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Q9X0L4;
                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                 CONFLICT
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                                                                                                                                                                                                                                                                             CHAIN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                        -!- SUBUNIT: HOMOTETRAMER.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE PHOSPHATE ACETYLTRANSFERASE AND
BUTYRYLTRANSFERASE FAMILY. MORE SIMILAR TO PTB THAN PTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-90237079; PubMed-2159010;
Yamada M., Amuro N., Goto Y., Okazaki T.;
"Structural organization of the rat cytochrome c oxidase subunit IV
FUNCTION: IN ADDITION TO ACETYL-COA (100%), THE ENZYME ACCEPTS PROPIONYL-COA (60%) AND BUTYRYL-COA (30%), HAS A TEMPERATURE OPTIMUM AT 90 DEGREES CELSIUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goto Y., Amuro N., Okazaki T.; "Nucleotide sequence of cDNA for rat brain and liver cytochrome \boldsymbol{c}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=WISTAR; TISSUE-Liver;
MEDLINE-89296488; PubMed-2544859;
Gopalan G., Droste M., Kadenbach B.;
Nucleotide sequence of cDNA encoding subunit IV of cytochrome oxidase from fetal rat liver:";
Nucleic Acids Res. 17:4376-4376(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                -i - PATHWAY: LAST OF TWO STEPS IN THE CONVERSION OF ACETATE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1989 (Rel. 11, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Cytochrome c oxidase polypeptide IV, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 294;
5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: Acetyl-CoA + phosphate - CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.3%; Score 48; DB
46.7%; Pred. No. 5.9;
Live 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oxidase subunit IV.";
Nucleic Acids Res. 17:2851-2851(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
MEDLINE-89240039; Pubmed-2541414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001770; AAD36206.1; -.
TIGR; TM1130; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002505; PTA_PTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |::: ||||:|: |
| 122 SVMEIPDEPRPLIIS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
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                                                                                                                                      phosphate.
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(BY SIMILARITY)
                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7653;
                                                                                                                                                  Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPC1_LYTPI
Q25378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lytechinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPC1_LYTPI
  QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                              MEDLINE-95324529; PubMed-7601105; Schaegger H., Noack H., Halanek W., Brandt U., von Jagow G.; Schaegger H., Noack H., Halanek W., Brandt U., von Jagow G.; Schaegger H., Noack H., Halanek W., Brandt U., von Jagow G.; Schaegger H., Noack H., Halanek W., Brandt D., Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform."; Eur. J. Biochem. 230:235-241(1995).

-!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
                                                                                                                                              Virbasius J.V., Scarpulla R.C., "The rat cytochrome c oxidase subunit IV gene family: tissue-specific and hormonal differences in subunit IV and cytochrome c mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                           Amuro N., Yamada M., Goto Y., Okazaki T.; "Complete nucleotide sequence of the gene encoding rat cytochrome c oxidase subunit IV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOCHROME C OXIDASE POLYPEPTIDE IV. F0187C76B7A1A9FE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; Mitochondrion; Transit peptide.
TRANSIT 1 22 MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                  Nucleic Acids Res. 18:6581-6586(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                 Nucleic Acids Res. 18:3992-3992(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
            Biol. Chem. 265:7687-7692(1990).
                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-91067442; PubMed-2174541;
                                  SEQUENCE FROM N.A.
MEDLINE-90326528; PubMed-2165254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X14209; CAA32426.1; -.
EMBL; X15029; CAA33133.1; -.
EMBL; J05425; AAA40049.1; -.
EMBL; X54081; CAA38018.1; -.
PIR; A35209; A35209.
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YALPSYVDRRDYPLPDVAHVKL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19514 MW;
                                                                                                                                                                                                                                      STRAIN-WISTAR; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004203; COX4. Pfam; PF02936; COX4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S12724; S12724.
PIR; S14190; S14190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                         SEQUENCE OF 23-32
                                                                                                                                                                                                                                                                                                                                                                             c + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P00423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEM3_CHLTR
084301;
                                                                                                                                                                                     expression.
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Probable porphobilinogen deaminase (EC 4.3.1.8) (PBG)
(Hydroxymethylbilane synthase) (HMBS) (Pre-uroporphyrinogen synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROXYMETHYLBILANE PREUROPORPHYRINOGEN IN SEVERAL DISCRETE STEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: 4 porphobilinogen + H(2)O = hydroxymethybliane + 4 NH(3).
-! hydroxymethybliane + 4 NH(3).
-!- PATHMAY: FOURTH STEP IN PORPHYRIN BIOSYNTHESIS BY THE C5 PATHMAY.
-!- SIMILARITY: BELONGS TO THE HMBS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Rakow T.L., Shen S.S.;
Rakow T.L., Shen S.S.;
"Molecular cloning and characterization of protein kinase C from the sea urchin Lytechinus pictus.";
Sea urchin Lytechinus pictus.";
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
SERINE- AND THREONINE-SPECIFIC ENZYME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lytechinus pictus (Painted sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                        Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
Science 282:754-759(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: TETRAPOLYMERIZATION OF THE MONOPYRROLE PBG INTO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó;
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SEQUENCE 241 AA; 26996 MW; F89FE00C20BF7044 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01379; Porphobil_deam; 1.
PROSITE; PS00533; PORPHOBILINOGEN_DEAM; FALSE_NEG.
                                                                                                                                   Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID-813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Protein kinase C (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P06983; 1AH5.
InterPro; IPR000860; Porphobil_deam.
                                                                                                                                                                                                                                                                                              STRAIN-D/UW-3/CX;
MEDLINE-99000809; PubMed-9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 CDLGIHSAKDLPENPKATVVSIT 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE001302; AAC67892.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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synthase II).
PURL OR PH1953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APT_SYNY3
P73935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APT_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
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                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bronpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS PHOSPHORYLATES A PROMOTERS (BY
                                               SIMILARITY).
SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAINS.
SIMILARITY: CONTAINS 1 C2 DOMAIN.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PURL PYRHO STANDARD; PRT; 705 AA.
205621;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phosphgribosylformylglycinamidine synthase II (EC 6.3.5.3) (FGAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                          RANKT; SW00109; TYRINASE.

S.MART; SW00109; C1; 2.

S.MART; SW00139; C2; 1.

S.MART; SW00131; CTK X; 1.

S.MART; SW00131; CTK X; 1.

S.MART; SW00131; CTK X; 1.

R. PROSITE; PS0004; C2_DOMAIN_2; 1.

R. PROSITE; PS0004; C2_DOMAIN_2; 1.

R. PROSITE; PS00010; PROTEIN_LNDA_1; 2.

R. PROSITE; PS50010; PROTEIN_LNDA_2; 2.

R. PROSITE; PS500110; PROTEIN_LNDSE_ATP; 1.

R. PROSITE; PS500110; PROTEIN_LNASE_ATP; 1.

R. PROSITE; PS500110; PROTEIN_LNASE_AT; 1.

R. MATP-binding; Transferase; Serine/threonine-protein kinase; Phorbol-ester binding; Zinc; Repeat.

R. DOMAIN 28 77 PHORBOL-ESTER AND DAG BINDING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING 1.
BINDING 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.9%; Score 46; DB 1; Length 658; 43.5%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74B5A27A49C835A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHORBOL-ESTER AND DAG
PHORBOL-ESTER AND DAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
                                                                                                                                                                                                                       send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2 DOMAIN
                                                                                                                                                                                                                                                                     InterPro; IPR000008; C2.
InterPro; IPR00219; DAG_PE-bind.
InterPro; IPR000719; Euk_Pkinase.
InterPro; IPR000561; Pkinase_C
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|||:: | :|| : | |:|:|
533 FQSIMEHVPSYPKSMSRESVTMC 555
                                                                                                                                                                                                                                                                                                                                                Pfam; PF00168; C2; 1.
Pfam; PF00130; DAG_PE-bind; 2.
Pfam; PF00139; pkinase; 1.
Pfam; PF00433; pkinase_C; 1.
PRINTS; PR000360; C2DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 YQSIVDR-PDFPKPIVR-SITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74871 MW;
                                                                                                                                                                                                                                               EMBL; U02967; AAA03447.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93
164
325
331
354
449
658 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                 PKC SUBFAMILY.
                                                                                                                                                                                                                                                             HSSP; P05697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PURL_PYRHO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA RES. 5:55-76(1998).
-!- CATALYTIC ACTIVITY: ATP + 5'-phosphoribosylformylglycinamide + L-glutamine + H(2)0 - ADP + phosphete + 5'-phosphoribosylformylglycinamidine + Lephosphoribosylformylglycinamidine + Lephosphoribosylformylglycinamidine + Lephosphoribosylformylglycinamidine + Lephosphoribosylformylglycinamidine + Lephosphoribosylformylglycinamidine + Lephosphoribosylformylglycinamidine + SUBCELULAR DECORTION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE FGAMS FAMILY.
                                                                                                                                                                                                                                              Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kibuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii Of3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-97061201: PubMed-8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Kanako T., Sato S., Rotani H., Tanaka A., Sasamoto S., Kimura T.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Hisosuchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,

Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,

Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Pyrococcus horikoshii.
Archaea: Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ligase, ATP-binding; Complete proteome.
10
8540 MW; 57550733AAA4DE29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 705; 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocystis sp. (strain PCC 6803),
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.9%; Score 46; DB 44.4%; Pred. No. 30; Live 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP000007; BAA31080.1; -.
InterPro; IPR000728; AIRS_related.
Pfam; PF00586; AIRS, 2.
Pfam; PF02769; AIRS_C; 2.
Purine biosynthesis; Ligase; ATP-bin
NP_BIND 89 100 ATP (PO'
SEQUENCE 705 AA; 78540 MW; 57550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                       MEDLINE-98344137; PubMed-9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY 2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequ
16-0CT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | |||:| ||:| :
513 YNEIVDKPIKPTPVVAGV 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 YQSIVDRPDFPKPIVRSI 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Construction of a contiguous 874-kb sequence of the Escherichia coli - K12 genome corresponding to 50.0-68.8~\mathrm{min} on the linkage map and analysis of its sequence features.";
           CATALYTIC ACTIVITY: (3S)-3-hydroxyacyl-CoA = trans-2(or 3)-enoyl-
                                          SIMILARITY: BELONGS TO THE ENOYL-COA HYDRATASE/ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satch Y., Sivasundaram S., Yamagata S., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=K12, / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUGG_ECOLI STANDARD; PRT; 907 AA.
P33602; P76489; P78184; P78185;
P13602; P76489; Rel. 28, Created)
15-JUJ-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADH dehydrogenase I chain G (EC 1.6.5.3) (NADH-ubiquinone oxidoreductase chain G) (NUO7).
                                                                                                                                                                                                                                                                                                                                                                                                                                  32.1%; Score 45; DB i; Length 294; 50.0%; Pred. No. 17; tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                          Pfam; PF00378; ECH; 1. Proceeds: PR0378; ECH; 1. PR051TE; PS00166; ENOYL_COA HYDRATAES; 1. Fatty acid metabolism; Lyase; Complete proteome. SEQUENCE 294 AA; 31491 MW; 0B7502E715A7D692 CRC64;
                                                                                                                                                                                                                                                                                           Leproma; ML1241; -.
InterPro; IPR001753; Enoyl_CoA_hydrtse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K12;
MEDLINE=97349980; PubMed=9205837;
                                                                                                                                                                                                                                     EMBL; AL049913; CAB43147.1; -. EMBL; AL583921; CAC31622.1; -. HSSP; P14604; 2DUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|: | |||:| | |||
15 YRSVTDLVVLDFPRPEVALITL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 YOSIVDRP--DFPKPIVRSITL 24
                                                                                                                                                                                                                        EMBL; U00010; AAA17070.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gregor J., Davis
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUOG OR B2283
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                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ή
MEDLINE-21128732; PubMed-11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simonds M., Selton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00103; PUR PYR PR TRANSFER; 1.
Transferase; Glycosyltransferase; Purine salvage; Complete proteome.
SEQUENCE 172 AA; 18997 MW; D577E94BCEF4E457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: COULD POSSIBLY OXIDIZES FATTY ACIDS USING SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith D.R., Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Probable enoyl-CoA hydratase echAl2 (EC 4.2.1.17).
ECHAl2 OR ML1241 OR MLCB1610.01 OR B1170_C2_224.
                                                                                                                                                SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYPODJASMIC.
SMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.1%; Score 45; DB 1; 61.1%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                            EMBL; D90911; BAA18001.1; -.
InterPro; IPR000836; Pribosyltran.
InterPro; IPR002375; Pur_pyr_br_transf.
Pfam; PF00156; Pribosyltran; 1.
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Best Local Similarity 61.1%
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Barrow P.A.;
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P33900;
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COFACTOR: BINDS 1 2FE-2S CLUSTER AND 1 4FE-4S CLUSTER (Potential).
SUBUNIT: COMPOSED OF 13 DIFFERENT SUBUNITS. SUBUNITS NOCCD, E,
F, AND, G CONSTITUTE THE PERIPHERAL SECTOR OF THE COMPLEX.
SIMILARITY: BELONGS TO THE COMPLEX I 75 kDa SUBUNIT FAMILY.
CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BELIEVED
                MEDLINE-93389724; PubMed-7690854; Weiblor U. Geler S., Ptock A., Friedrich T., Leif H., Weiss H.; Weidner U., Geler S., Ptock A., Friedrich T., Leif H., Weiss H.; arthe gene locus of the proton translocating NAH: ubiquinone oxidoreductase in Escherichia coll. Organization of the 14 genes and relationship between the derived proteins and subunits of mitochondrial complex I. amiltochondrial complex I. a. Mol. Biol. 233:109-122(1993).
                                                                                                                                                                                                                                                                                                                                                   MEDITIE—97443975; PubMed-9298646;
Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
-!- FUNCTION: TRANSFER OF ELECTRON ACCEPTOR FOR THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED TO BE UBIQUINONE. DOES COUPLE THE REDOX REACTION TO PROTON TRANSLOCATION AND THUS CONSERVES THE REDOX ENERGY IN A PROTON TRANSLOCATION AND THUS CONSERVES THE REDOX ENERGY IN A PROTON
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MEDLINE=94209210; PubMed=8157582;
Pruss B.M., Nelms J.M., Park C., Wolfe A.J.;
"Mutations in NADH:ubiquinone oxidoreductase of Escherichia coli affect growth on mixed amino acids.";
J. Bacteriol. 176:2143-2150(1994).
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PROSITE; PS00642; COMPLEX1_75K_2; 1.
PROSITE; PS00643; COMPLEX1_75K_3; 1.
Oxidoreductase; NAD; Ubiquinone; Iron-sulfur; 4Fe-4S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; Pubbed-11677609; MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latrellle P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulyaney E., Ryan E., Sun H., Florea L., Milier W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium
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SPECIES-S. typhimurium;
MEDLINE-94052195; PubMed-8234329;
Archer C.D., Wang X., Elliott T.;
"Mutants defective in the energy-conserving NADH dehydrogenase of Salmonella typhimurium identified by a decrease in energy-dependent protecolysis after carbon starvation.";
Proc. Natl. Acad. Sci. U.S.A. 90:9877-9881(1993).
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SPECIES-S. Lyphimurium; STRAIN-F98;
MEDLINE-98037511; Pubmed-9971470;
Zhang-Barber L.Z., Turner A.K., Martin G., Fraenkel G., Dougan G.
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U-MRR-2002 (Rel. 41, Last sequence update)
01-MRR-2002 (Rel. 41, Last annotation update)
NADH dehydrogenase I chain G (EC 1.6.5.3) (NADH-ubiquinone oxidoreductase chain G) (NVO7).
NUCG OR STM2323 OR STY2553.
Salmonella typhimurium, and
                                                                                                                                                                                              Length 907
209 T -> K (IN REF. 3).
389 MISSING (IN REF. 3).
47 S -> T (IN REF. 3).
100168 MW; 4C258FEEF3533F2 CRC64;
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                                                                                                                                                                                              Score 45;
Pred. No.
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57.1%;
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Best Local Similarity 57.1.
8: Conservative
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268 GYGYVNLKDRPRQP 281
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607 AA;
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                                                                     I- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE BUXYME IS BELIEVED TO BE UBIQUINONE. DOES COUPLE THE REDOX REACTION TO PROTON TRANSLOCATION AND THUS CONSERVES THE REDOX BERGY IN A PROTON
                                                                                                                                                                                                             -:- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-:- COFACTOR: BINDS 1 2FE-2S CLUSTER AND 1 4FE-4S CLUSTER (Potential).
-:- SUBUNIT: COMPOSED OF 13 DIFFERENT SUBUNITS. SUBUNITS NUOCD, E,
F, AND, G CONSTITUTE THE PERIPHERAL SECTOR OF THE COMPLEX.
-:- SIMILARITY: BELONGS TO THE COMPLEX I 75 kDa SUBUNIT FAMILY.
-:- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
FRAMESHIFTS IN POSITIONS 714 AND 805.
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enterica serovar Typhi CT18.";
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                                                Nature 413:848-852
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Indels

Pred. No. 56; 2; Mismatches

Conservative

Query Match Best Local Similarity Matches 8; Conserv

32.1%; Score 45; 57.1%; Pred. No.

DB 1; Length 907;

Search completed: August 26, 2002, 10:17:03 Job time: 699 sec

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Perfect score:

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Sequence:

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Database

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09cb84 mycobacteri
09cs0 bothriochlo
09v83 drosophila
09vr8 drosophila
09nr8 drosophila
09nf8 drosophila
09nf8 drosophila
09nf9 drosophila
09f10 moultured
0914b7 uncultured
0914b7 uncultured
0911t0 mus musculu
09cl10 mus musculu
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09hwd2 pseudomonas
015882 trypanosoma
09xcf5 mycobacteri
09ve06 drosophila
09yla8 drosophila
        Q12204 saccharomyc
Q98101 rhizobium 1
Q94gf6 oryza sativ
Q96wv1 schizosacch
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                                          094bp2 arabidopsis
09w6b2 xenopus lae
09an61 bradyrhizob
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P72628 synechocyst
Q10667 caenorhabdi
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Pred. No. 8.2;
6; Mismatches 7; Indels 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003492; BAB61859.1; --
SEQUENCE 460 AA; 49420 MW; 549DD3183A0408B6 CRC64;
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STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
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        Q12204
Q98I01
Q94GF6
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Q9XCF5
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Best Local Similarity 37.9%;
Matches 11; Conservative (
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NCBI_TaxID=4530;
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Q94D33;
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099711 deinococcus
099917 drosophila
099825 lampetra ja
099801 hizobium 1
091925 xenopus lae
040983 pisum sativ
058856 beet yellow
058856 beet yellow
059496 drosophila
099496 drosophila
099496 satabidopsis
093464 escherichia
069727 mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q94d33 oryza sativ
Q27123 urechis cau
                                                                    (without alignments)
64.724 Million cell updates/sec
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                                                            August 26, 2002, 10:16:19 ; Search time 66.82 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                              562222
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                           562222 seqs, 172994929 residues
                                                                                                              CGYGYQSIVDRPDFPKPIVRSITLC 25
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                                                                                                                                                                                                                                          Listing first 45 summaries
                                          OM protein - protein search, using sw model
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027123
093701
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040925
065856
0920W6
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_invertebrate:*
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sp_phage:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 200000000
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182
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711
711
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Match
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Score

Result Š 52.5 51.5 449 488.5 488 488 488

46.5 46.5 46.5 46

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CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                   radiodurans Rl.
                                                                                                                                                 Fraser C.M.;
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                                                                                       Rosenthal E.; "Sequence analysis of translationally controlled maternal mRNAs from
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99044580; PubMed=9827331;
She Q., Phan H., Garrett R.A., Albers S.V., Stedman K.M., Zillig
"Genetic profile of pNOB8 from Sulfolobus: the first conjugative
plasmid from an archaeon.";
Extremophiles 2:417-4251998).
EMBL; AJ010405; CAA09149.1;
                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus. NCBL_TaxID=84600;
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                            Urechis caupo (Innkeeper worm) (Spoonworm).
Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
                                                                                                                                                                                                                              Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49; DB 1; Length 165;
Pred. No. 9.5;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                Indels
                                                                                                                                                 Rosenthal E.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
SIB: AAA74396.1; -
InterPro; IPR004203; COX4.
                                                                                                                                                                                                CC8EC1FA5F84D766 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Plasmid.
SEQUENCE 165 AA; 19189 MW; 22E6A92532874A80 CRC64;
                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
          Last annotation update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation updat CYTOCHROME C OXIDASE SUBUNIT IV.
                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                            Score 51.5; DB 5;
Pred. No. 4.5;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                       165 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                   SEQUENCE FROM N.A.
MEDLINE-94155469; PubMed-8111976;
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                                                                                                                                                                                                                                                                             48 GYGMNGLPTYIDLPEFPAPAVR 69
                                                                                                                                                                                                                                                                   2 GYGYQSI---VDRPDFPKPIVR 20
                                                                                                                                                                                      Pfam; PF02936; COX4; 1.
SEQUENCE 186 AA; 21084 MW;
                                                                                                                                                                                                                                                                                                                                                                                       KDA PROTEIN
                                                                                                                    Dev. Genet. 14:485-491(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.0%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, C
(TrEMBLrel. 13, I
(TrEMBLrel. 17, I
                                                                                                                                                                                                                             Query Match 36.8%;
Best Local Similarity 45.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
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                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus sp. NOB8H2.
Plasmid pNOB8.
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                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL 19.2
                                                 NCBI_TaxID=6431;
                                                                                                           Jrechis caupo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-NOBBH2;
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01-MAY-2000
01-JUN-2001
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Best Local Simi
Matches 10;
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Amanatides P.G. Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G. Scherer S.E., Holf R.A., Hoskins R.A., Galle R.F.,
Gocage R.A., Lewis S.E., Holf R.A., Hoskins R.A., Galle R.F.,
Gocage R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandall M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
M. Man K. H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Mikklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
A cherry J.M., Cawley S., Dahlke C., Devenport L.B., Davies P.,
A bodson K., Doug L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
A burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                              MEDLINE-20036896; PubMed-10567266;
White O., Eisen J.A., Heldelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                433 AA; 46392 MW; 9089C90957FE4465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001993; Mitoch_carrier.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1449 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     radiodurans Rl.";
Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE002019; AAF11328.1;
TIGR; DR1773; -.
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117 EAVAQRPDLPEPLLRQL 133
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Best Local Similarity
The 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 433 AA;
                                                                                                                               SEQUENCE FROM N.A.
                                                            NCBI_TaxID=1299;
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SEQUENCE FROM N.A.
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Q98MD1;
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         pp
Kammel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lakmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Lil J., Liz Z., Linang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Lil J., Liz Z., Linang Y., Lin X., R. Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mannt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Melson K., Nianon K., Niaskern D.R., Peacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ranner K., Kemignton K., Saunders R.D.C., Scheelber F., Shen H., Raine B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Sant M. Spier E., Wang X., Wang Z.-Y., Wassarman D.A., Umber R., Wenter E., Wang X., Mannt Z., Stapleton M., Strong R., Saunders S., Yao Q.A., R. Walliams S. M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., R. Zhong X.H., Zhong F.W., Zhong W., Zhang G., Zhao Q., Zheng L., R. Zhong F.W., Zhong W., Zhang G., Zhao Q., Zheng T., The genome sequence of Drosophila melanogaster.";

Rubis Applase; Feggnoodalge Cache.

Riberro; Iprolofold Cache.

Riberro; Iprolofold Cache.

Riberro; Iprolofold Cache.
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Endo Y., Takahashi M., Nakao M., Saiga H., Sekine H., Matsushita M.,
Nonaka M., Fujita T.;
"Two lineages of monose-binding lectin-associated serine protease
(MASP) in vertebrates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Immunol. 161:4924-4930(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MANNOSE-BINDING LECTIN-ASSOCIATED SERINE PROTEASE.
Lampetra japonica (Japanese lamprey) (Entosphenus japonicus)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lethenteron.
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                                                                                                                                                                                                                                                                                                                                                                                                                              35.0%; Score 49; DB 5; Length 1449; 33.3%; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                    550234; VWFA; 1.
1449 AA; 162090 MW; 70E3A155C4185D74 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRYPSIN FAMILY.
-! SIMILARITY: CONTAINS 2 CUB DOMAINS.
EMB!, AB009075; BAA86668.1; -.
HSSP; P00763: 11nn
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InterPro; IPR001881; EGF_Ca.
InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR001254; Trypsin.
Pfam; PF00431; CUB; 2.
Pfam; PF00084; sushi; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 35.0°
Best Local Similarity 33.3°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02743; Cache; 3.
                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50234; VWFA; SEQUENCE 1449 AA; 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=94989;
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REPURS: PRO0722: CHYMOTRYPSIN, 1.

REPURS: SMO0722: CHYMOTRYPSIN.

REPURS: SMO0122: CCP: 2.

REPURS: SMO0122: CCP: 2.

REPURS: SMO0179: ECF.CA; 1.

REPURS: SMO0100; ASX_HYDROXYL; UNKNOWN_1.

REPURS: PS01180: CCP: 2.

REPURS: PS01180: ECF.CA; 1.

REPURS: PS01187: ECF.CA; 1.

RE
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MEDLINE-21082930; PubMed-11214968;
Kaneko T., Nakamura Y., Sato S., Sato S., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Matsuno A., Takeuti Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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Pred. No. 55;
4; Mismatches 7; Indels 21
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Pred. No. 68;
2; Mismatches 5; Indels
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Last annotation update)
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DNA Res. 7:331-338(2000).
EMBL; AP002995; BAB48182.1; -.
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53.3%;
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Best Local Similarity 25.6%;
Matches 11; Conservative
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01-NOV-1996 (TrEMBLEEL.
01-NOV-1996 (TrEMBLEEL.
01-DEC-2001 (TrEMBLEEL.
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Best Local Similarity
Matches 8; Conserv
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Kenopus laevis (African clawed frog).

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                                                                            5,
                                                                                                                                            79 YSSVLSQPTAPVPVRQSCTSC 99
                                       34.3%;
38.1%;
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                                                                                                                     5 YQSIVDRPDFPKPIVRSITLC
                                                                              Conservative
                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                               Beet yellow stunt virus
                                       Query Match
Best Local Similarity
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Q65856;
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SMART; SM00042; CUB; 5.
SMART; SM00179; EGF_CA; 2.
SMART; SM00135; ZuAC; 1.
PROSITE; PS00010; ASX HYDROXYL; 2.
PROSITE; PS01180; CUB; 5.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01142; ZINC_PROPEASE; UNKNOWN_1.
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SEQUENCE 977 AA; 110199 MW; 4D7D2E37C64FDFIF CRC64;
                                                                                                                                                      Pisum satirum (Garden pea).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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MEDLINE-95365331; PubMed=7638164;
VanderVere P.S., Bennett T.M., Oblong J.E., Lamppa G.K.;
VanderVere P.S., Bennett T.M., Oblong J.E., Lamppa G.K.;
VanderVere P.S., Bennett With a recently recognized family of an anetalloendopeptidases. ";
Proc. Natl. Acad. Sci. U.S.A. 92:7177-7181(1995).

EMBL; U25111; AAA81472.1;

MÉROPS; M16.004;
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBL_TaxID=835;
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SEQUENCE 1259 AA; 139573 MW; 5DBB33ED0D123B3F CRC64;
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Last sequence update)
Last annotation update)
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Pred. No. 90;
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                                                                                                                                                                                                                                                                                                           InterPro; IPR001506; Astacin.
InterPro; IPR00152; Asx_hydroxyl.
InterPro; IPR000859; CUB.
InterPro; IPR0008561; EGF-1ike.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR00130; Zn_MTpeptdse.
Pfam; PF01400; Astacin; 1.
Pfam; PF00008; EGF; 2.
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47.18;
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Best Local Similarity
Matches 8; Conserva
                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                      TISSUE-EMBRYO;
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EMBL: U51931; AAC55663.1; SEQUENCE 534 AA.
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MEDLINE-21396508; PubMed=11481431;
MEDLINE-21396508; PubMed=11481431;
MEDLINE-21396508; PubMed=11481431;
MEDLINE-21396508; PubMed=11481431;
Worlocater F.J., Hernandez-Luca I., Becker A., Cowle A., Gouzy J., Golding B., Puchler A.;
Golding B., Puchler A.;
"The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meillott.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karasev A.V., Nikolaeva O.V., Mushegian A.R., Lee R.F., Dawson W.O.; "Organization of the 3'-terminal half of beet yellow stunt virus genome and implications for the evolution of closteroviruses."; Virology 221:199-207(1996).
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Karasev A.V., Nikolaeva O.V., Lee R.F., Wisler G.C., Duffus J.E.,
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE ACETOLACTATE SYNTHASE ISOZYME I LARGE SUBUNIT PROTEIN
Length 1259;
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Last annotation update)
Score 48; DB 10;
Pred. No. 1.2e+02;
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Rhizoblum meliloti (Sinorhizoblum meliloti).
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                                                                  Mismatches
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RESULT 14
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                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                             Gaps
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                                                                                         Length 591;
                                                                                                                         Indels
                      Lyase; Plasmid; Hypothetical protein; Complete proteome. SEQUENCE 591 AA; 64157 MW; 7234D44FB221EB97 CRC64;
                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 19, Last annotation update)
                                                                                       33.6%; Score 47; DB 16;
52.6%; Pred. No. 75;
tive 1; Mismatches 4;
                                                                                                                                                                                                                                                                         182 AA
                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                            433 CGYGFPSIVGAKIGCPDVP 451
EMBE; AL603645; CAC49370.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 287:2185-2195(2000).
                                                                                                                                                        1 CGYGYQSIVDR----PDFP 15
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                                                                                                                                                                                                                                                                                                                                                        CG10664 PROTEIN (GM14452P)
                                                                                     Query Match
Best Local Similarity 52.6'
Matches 10; Conservative
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01-DEC-2001
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Gaps
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MEDLINE-20036896; PubMed-10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffatk K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBL_TaxID=1299;
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                                                                                                                                                                                                                                       Length 182;
                                                                                                                                                                                                                                                                          Indels
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SEQUENCE 210 AA; 22978 MW; 326EECF600C867E6 CRC64;
                                                                                                                                                                                  6D5953D8DE41217A CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILARITY TO UNKNOWN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Pred. No. 26;
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G
                                                                                                                                                                                  20519 MW;
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                                                                                                                                                                                                                                   33.2%;
nilarity 45.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 286:1571-1577(1999).
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                                                                                                                                                        Pfam; PF02936; COX4; SFRIENCE 182 AA;
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC clones.";
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Sloan J., Hartland E.;
Sloan J., Hartland E.;
"Putative transfer region (partial) and type IV pilus operon encoded by the large virulence plasmid, poll3, of enterohemorrhagic Escherichia coli 0113:H21.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF422146; AAL18824.1; -.
Blasmid.
SEQUENCE 206 AA; 22355 MW; DED02904AB24C87A CRC64;
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                                                                                 STRAIN=COLUMBIA;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.2%; Score 46.5; DB 10; Length 711; Best Local Similarity 33.3%; Pred. No. 1.1e+02; Matches 8; Conservative 5; Mismatches 6; Indels 5
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Pred. No. 35;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                          ATP-binding; Transferase.
SEQUENCE 711 AA; 81868 MW; AE31C91CA24F8AEO CRC64;
                                                                                                                                                                                       EMBL; AB025635; BAB08932.1; -...
EMBL; AB025635; BAB08932.1; -...
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR002096; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR002090; Ser_thr_pkinase.
InterPro; IPR002190; Ser_thr_pkinase.
InterPro; IPR002190; Ser_thr_pkinase.
InterPro; IPR002190; Tyrc; 1.
INTERPORTE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_I.
INTERPORTE; PS006011; PROTEIN_KINASE_DOM; 1.
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Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, C:
01-DEC-2001 (TrEMBLrel. 19, Ls
01-DEC-2001 (TrEMBLrel. 19, Le
PUTATIVE OXIDOREDUCTASE.
Escherichia coli.
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43.8%;
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Best Local Similarity 43.89
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Q93AF4
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Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglopenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylactic; anti-asthmatic; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Optimised IgE-CH3 domain antigen peptide for mouse IgE.
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                                                             AAY80080
AAY80084
AAY79998
AAY91212
                                                                                                                               AAY68602
AAY80014
AAY91215
AAY91216
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AAY68604
AAY68607
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AAY68605
AAY80011
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AAB06207
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99WO-US13959
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Synthetic.
 AAY80001;
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RESULT
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Optimised IgE-CH3
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2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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5: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
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110: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
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121: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
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33.557 Million cell updates/sec
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                                                                                                            August 26, 2002, 10:07:02; Search time 82.75 Seconds
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                                Compugen Ltd
                                                                                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
               GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                            747574 seqs, 111073796 residues
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antigenic peptide from the CH3 domain of immunoglobulin E, fusions immunization against allergy $\,^{\text{-}}$

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Result Š (UNBI-) UNITED BIOMEDICAL INC.

Wang CY, Walfield AM; WPI; 2000-160578/14.

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                                                                                                                                                                                    Sequence
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                                              antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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                                      the present invention describes immunoglobulin E (IgE)-CH3 domain
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            Claim 1; Page 100; 155pp; English.
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and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against igE-mediated allergies, e.g. food allergies, sathma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. ARY79994 to AAR80084 represent amino acid sequences used in the exemplification of the present invention.
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Pred. No. 7.8e-13;
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92.0%;
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Best Local Similarity
Matches 23; Conserv
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(functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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/label- immunoglobulin_E_heavy_chain
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Pred. No. 8e-13;
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                                                                                                                                                                                                                                                                                                                                                                                              Mouse immunoglobulin E heavy chain.
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Matches 23; Conservative
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95.5%; Pred. No. 2.1e-09;
tive 0; Mismatches 1;
Score 116; DB 20;
Pred. No. 1.4e-09;
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Matches 21; Conservative
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Matches 21; Conservative
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                                                                                                                                                                                                                               409967293-A1
                                             15-MAY-2000
                                                                                                                                                                                                                                                              29-DEC-1999.
                                                                                                                                                                                                 Rattus sp.
               AAY79996;
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                                                                                                                                                                                                                                                                                                                                                                                             Wang CY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic spetides (1). (1) have anti-allergic, anti-anaphylactic and antigenic peptides (1). (1) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (1) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (1) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                            Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobulin immunostimulatory; carrier protein; helper T cell epitope; antibody; allergic disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                              Optimised IgE-CH3 domain antigen peptide for rat IgE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 106; DB 21;
Pred. No. 1.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 99; 155pp; English.
191 gygyqcivdrpdfpkpivrsit 212
                                                                             AAY80000 standard; Peptide; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNBI-) UNITED BIOMEDICAL INC
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80.0%;
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                                                                                                                                               (first entry)
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Best Local Similarity 80.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang CY, Walfield AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-160578/14.
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Synthetic.
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ID AAY7
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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-alergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and
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                                                                                                          immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy \boldsymbol{\cdot}
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                                                                            immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
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Pred. No. 4.9e-05;
); Mismatches 5; Indels
Rat immunoglobulin E epsilon heavy chain SEQ ID NO:3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 66-68; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB03643 standard; protein; 340 AA.
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Best Local Similarity 77.3%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0100287.
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Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglopenic; immunosfimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylactic; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyroloal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils
                                                                                                                                                                                                The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant regions 1 from the rat. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigenic peptide from the CH3 domain of immunoglobulin E, fusions immunization against allergy \,^{\circ}
                                                                                                    Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin \boldsymbol{E} in mammals .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes immunoglobulin E (IqE)-CH3 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 341;
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                                                                                                                                                                  Disclosure; Fig 2; 50pp; English.
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Best Local Similarity 77.3%;
Matches 17; Conservative (
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                       Hellman LT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2, 3 and 4 of the rat IgE. It was used to construct a number of immunogenic peptides which consisted of regions of IgE from different mammals, which appear to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic peptide consisting of opossum CH2, rat CH3 and opossum CH4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          \ensuremath{\mathsf{Immunogenic}} polypeptides useful for preventing the harmful effects \ensuremath{\mathsf{Immunoglobulin}} E in mammals -
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Rat; immunoglobulin E; IgE; vaccination; infection; allergy; asthma; eczema; immunogenic peptide.
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Chimeric - Rattus sp.
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99US-0401636.
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Matches 17; Conserv
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22-SEP-1999;
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22-SEP-1999;
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                                                         Rattus sp.
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                containing (I) are used for active immunisation against IgE mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent anno acid sequences used in the exemplification of the present invention.
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antibody; allergy; allergic disease; immunisation; anti-allergic;
anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
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  downregulation of IgE synthesis. Conjugates, or fusion peptides
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Pred. No. 0.00015;
3; Mismatches 9; Indels
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52.0%;
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                                                                                                                                                                                                                                                                                                                                   Local Similarity
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Synthetic.
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antigenic peptides (I). (I) have anti-allergic anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies and anti-asthmatic properties. (I) induces polyclonal antibodies are persilve for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. (conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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               target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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(functional in genetically diverse subjects), in addition to a B cell
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                                                                                                                                                                                                     Score 66; DB 21; Length 25; Pred. No. 0.0027; 0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                  AAY80019 standard; Peptide; 45
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1 Similarity 56.0%;
14; Conservative
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Best Local Similarity
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CGYGYQSIVDRPDFPKPIVRSITLC

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                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglopatic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy disease; immunisation; anti-allergic; anti-acthmatic; asthma; anaphylaxis; dermatitis.
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                                                   Score 66; DB 21; Length 45;
Pred. No. 0.0051;
0; Mismatches 11; Indels
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                                                                                                                          1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                             for immunization against allergy
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56.08;
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                                                    Query Match 47.18
Best Local Similarity 56.08
Matches 14; Conservative
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45 AA;
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The present invention describes immunoglobulin E (IgE)-CH3 domain antigaric peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epicope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and
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                                                                                                                                                                                                                                                                              immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
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                                                                                                                                                                                                                         IgE immunogenic peptide conjugate SEQ ID NO:27.
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                                                                                                              46 AA
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                                                                                                          AAY80020 standard; Peptide;
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Matches 14; Conservative
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47.1%; Score 66; DB 21; Length 45; 56.0%; Pred. No. 0.0051; tive 0; Mismatches 11; Indels

Conservative

Best Local Similarity Matches 14; Conserv

Query Match

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antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-athmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the spalion heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthum, anaphylaxis, or flea-allergy dermathis. Nucletc acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. (conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                               Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; himmunoglopalıc; immunoglimlatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
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                                                                                                                        IgE immunogenic peptide conjugate SEQ ID NO:88.
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AAY80081 standard; Peptide; 57 AA.
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Query Match 47.1%; Score 66; DB 21; Length 57; Best Local Similarity 56.0%; Pred. No. 0.0067; Matches 14; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

1 CGYGYQSIVDRPDFPKPIVRSITLC 25

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33 cgetyysrvthphlpkdivrsiakc 57

Search completed: August 26, 2002, 10:07:02 Job time: 228 sec

Perfect score:

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Run

Scoring table: Sequence:

Database

Result No.

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US-09-192-545-2

Sequence 2, Application US/09192545

Patent No. 6118044

GENERAL INFORMATION:
APPLICANT: Karasuyama, Hajime
APPLICANT: Yonekawa, Hiromichi
APPLICANT: Tonekawa, Hiromichi
APPLICANT: Taya, Choji
APPLICANT: Taya, Choji
APPLICANT: Taya, Choji
APPLICANT: Taya, Choji
CURRENT APPLICATION NUMBER: US/09/192,545

CURRENT APLICATION NUMBER: US/09/192,545

CURRENT FILING DATE: 1998-11-13

EARLIER FILING DATE: 1998-11-14

NUMBER OF SEQ ID NOS: 12

SOCTHARE: PatentIN Ver. 2.0

SEQ ID NO 2

LENGTH: 561
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Best Local Similarity 91.3%; Pred. No. 7.7e-10;
Matches 21; Conservative 1; Mismatches 1;
US-09-187-859-33
US-08-225-539D-56
US-08-103-45-4
US-08-461-6908-4
US-08-486-342-2
US-08-473-092-2
US-08-66-371-2
US-09-042-494-2
US-09-0413-814-50
US-09-413-814-50
US-08-470-56-874-2
US-08-877-698-2
US-08-775-0145-18
US-08-771-0145-18
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Sequence 95, Application US/09100414B
Sequence 95, Application US/09100414B
Sequence 95, Application US/09100414B
Sequence 95, Application US/09100414B
SEMERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.
STREET: 345 Park Avenue
CITY: New York
STARET: NY
STARET: NY
STARET: USA
COUNTRY: USA
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FEATURE: Description
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Sequence 98, Appl
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Sequence 100, Appl
Sequence 99, Appl
Sequence 101, Appl
Sequence 101, Appl
Sequence 96, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 102, Appl
Sequence 102, Appl
Sequence 102, Appl
Sequence 102, Appl
Sequence 103, Appl
Sequence 113, Appl
Sequence 113, Appl
Sequence 113, Appl
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(without alignments)
17.865 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                                    Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-303-323-95
US-09-100-414B-98
US-09-100-414B-99
US-09-303-323-98
US-09-303-323-99
US-09-303-323-99
US-09-100-414B-101
US-09-100-414B-96
US-09-100-414B-97
US-09-100-414B-97
US-09-100-414B-97
US-09-100-414B-102
US-09-10
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US-09-461-474-2
US-08-232-539D-54
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US-08-818-823-2
                           GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                              1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                   231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein • protein search, using sw model
                                                                                                                                                                 August 26, 2002, 10:05:18
                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                               us-09-701-623C-8
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Match Length
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                                                                                                     45.7%; Score 64; DB 4; Length 25; 48.0%; Pred. No. 0.0021; tive 3; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 99, Application US/09100414B
Sequence 99, Application US/09100414B
Sequence 99, Application US/09100414B
Sequence 99, Application US/09100414B
Fatent No. 602546B
Sequence 99, Application US/09100414B
Fatent No. 602546B
TITLE OF INVENTION: IMMUNOGENS
TITLE OF INVENTION: IMMUNOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 98:
                                                                                                                                                                                                                                                                                               1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC Windows SOFTWARE: Word 97 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/100, FILING DATE: 20-JUNE-1998 CLASSIFICATION: 424 ATTONNEY AGGNT INFORMATION: NAME: MAILA H. LIN REGISTRATION NUMBER: 29,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CGYGYQSIVDRPDFPKPIVRSITLC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.09
Matches 12; Conservative
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                                                                                                       Query Match
Best Local Similarity 48.0°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
                            ; MOLECULE TYPE: peptide US-09-303-323-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide US-09-100-414B-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
            linear
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            TOPOLOGY:
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Pred. No. 0.0021;
3; Mismatches 10; Indels
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Fatent No. 6228987
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESSE:
ADDRESSEE: MOTGAN & Finnegan, L.L.P.
STREET: 345 Park Avenue
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY, ARGENT INFORMATION:
NAME: MARIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-751-6849
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1151-4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PULICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILLING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 48.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 25 amino acids TYPE; amino acid
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-100-414B-95
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STATE: NI
COUNTRY: USA
TO: 10154-0054
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US-09-303-323-95
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                                                                                                                                                                                           45.7%; Score 64; DB 3; Length 42;
48.0%; Pred. No. 0.0038;
tive 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LIRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10154-0054
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29,323
FR: 1151-4157
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FILING DATE: 30-APR-122.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAZIA H. Lin
REGISTRATION NUMBER: 29,323
REPERENCE/POCKET NUMBER: 1151-4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGYGYQSIVDRPDFPKPIVRSITLC 25
    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                             Query Match
Best Local Similarity 48.0°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                 ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-09-100-414B-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 12; Conserva
                                                                      TYPE: amino acid
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GY: linear
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US-09-303-323-99
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STATE:
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Fatent No. 6025468
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: INMUNOCENS
INTER OF INVENTION: INMUNOCENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
STREET: 345 Park Avenue
CITY: New York
STRAFE: NY
COUNTRY: USA
INFORMATION: COMPATION:
COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION:
MEDIUM TYPE: LOPPY disk
COMPUTER: IBM PC COMPATION:
MEDIUM TYPE: 20-JUNE-1998
CLASSIFICATION NUMBER: US/09/100, 414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 213-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-751-6849
                                                                                                                  COUNTY: USA

ZIP: 10154-0054

ZIP: 10154-0054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELEFRONE: 212-751-6849
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                           USA
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                                                                                                           COUNTRY:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 101, Application US/09100414B
Patent NO. 6025468
GENERL INFORMATION:
TITLE OF INVENTION: IMMUNOGENS
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
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      US/09/303,323
                                                      PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/100,414

FILLIG DATE: 20-JUNE-1998

ATTORNEY/AGENT INFORMATION:

NAME: Maria H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-41:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-751-684800

INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARATTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFRENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 101:
                        30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 45.7%
Best Local Similarity 48.0%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                      LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-09-303-323-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide US-09-100-414B-101
        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                              linear
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                                            CLASSIFICATION:
                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-100-414B-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.7%; Score 64; DB 4; Length 42; llarity 48.0%; Pred. No. 0.0038; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 100, Application US/09303323
Sequence 100, Application US/09303323
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
Sequence 99, Application US/09303323
Fatent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                          ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1151-4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MARIA H. LIN
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-415
TELEPHONE: 212-758-4800
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: WORD 97
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 99: SEQUENCE CHARACTERISTICS: LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide US-09-303-323-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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STATE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WOLD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-758-4800
TELECHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MAITA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 97, Application US/09100414B Patent No. 6025468 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 CGETYQSRVTHPHLPRALMRSTTKC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                       PC Windows
                                                                                                               E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-,... 9t
INFORMATION FOR SEQ ID NO: 9t
SEQUENCE CHARACTERISTICS:
""NOTH: 46 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELERAX: 212-7.2.
INFORMATION FOR SEQ ID NO: 97
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 48.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide US-09-100-4148-96
                                                                      ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                       Word 97
                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Word 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10154-0054
                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-100-414B-97
                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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Best Local Similarity 48.0%; Pred. No. 0.004; Matches 12; Conservative 3; Mismatches 10; Indels
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                                                                                                                                                                                 US-00-303-323-101

Sequence 101, Application US/09303323

Patent No. 6228987

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: NOVEL LHRH PEPTIDE

TITLE OF INVENTION: IMMUNOGENS

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 96, Application US/09100414B
; Sequence 96, Application US/09100414B
; Patent No. 602546B
; GENERAL INFORMATION:
    APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR PAPLICATION DATA
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC Windows SOFTWARE: Word 97 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/303,323 FILING DATE: 30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                        CITY.
STATE: NY
COMPRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"AMDIUM TYPE: Floppy disk
"AMDIUM TYPE: Floppy disk
"AMDIUM TYPE: Floppy disk
                                                                    1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                             21 CGETYQSRVTHPHLPRALMRSTTKC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 CGETYQSRVTHPHLPRALMRSTTKC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-751-6849 INFORMATION FOR SEQ ID NO: 101:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.09
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-09-303-323-101
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Query Match
45.7%; Score 64; DB 4; Length 46;
Best Local Similarity 48.0%; Pred. No. 0.0041;
Matches 12; Conservative 3; Mismatches 10; Indels
TITLE OF INVENTION: NOVEL LHRH PEPTIDE TITLE OF INVENTION: NOVEL LHRH PEPTIDE TITLE OF INVENTION: IMMUNGENS NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
STREFT: E. MOTGAR
                                                                                                                                                             ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
2.IP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-UNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MARIA H. LÎN
REGISFATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: August 26, 2002, 10:05:19 Job time: 125 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPHAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 CGETYOSRVTHPHLPRALMRSTTKC 46
                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-09-303-323-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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                                                                                                                                                                                         Score 64; DB 3; Length 46;
Pred. No. 0.0041;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-303-323-96
Sequence 96, Application US/09303323
Patent NO. 6228947
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCES: 106
CORRESPONDENCES: 106
CORRESPONDENCES: 106
CORRESPONDENCES: 106
CORRESPONDENCES: 106
CORRESPONDENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITT: New YORK
STRTE: NY
COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TIPE: ELOPPY OISK
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: WOR'D 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION: DATA: APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MARIA H. LIN
RECISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-758-4809
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTER/STICS:
TELECHONE: AMAIO ACIDS
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTER/STICS:
TELECHONE: AMAIO ACIDS
                                                                                                                                                                                                                                                                                1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 CGETYQSRVTHPHLPRALMRSTTKC 46
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; Sequence 97, Application US/09303323
; Patent No. 6228987
                                                                                                                                                                                       Query Match
Best Local Similarity 48.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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Best Local Similarity 48.05
Matches 12; Conservative
                                                   ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-4148-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-09-303-323-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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Search time 45.87 Seconds (without alignments) 52.370 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                    August 26, 2002, 10:04:23;
                                                                                          - protein search, using sw model
                                                                                       OM protein
                                                                                                                                    Run on:
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25 141 1 CGETYYSRVTHPHLPKDIVRSIAKC US-09-701-623C-6 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283138 Total number of hits satisfying chosen parameters: 283138 seqs, 96089334 residues

Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Iq epsilon-chain -	Ig epsilon chain C	Ig epsilon chain C	IgE chain C3 regio	IgE chain C3 regio	Ig epsilon chain C	Ig epsilon chain C	hypothetical prote	hypothetical prote	Ca	acetyl-CoA carboxy	acetyl-CoA carboxy	acetyl-CoA carboxy	hypothetical prote	alpha-fetoprotein	hypothetical prote		_	Ω,	gas-vesicle protei	gas-vesicle operon	novel antigen rece	acetyl-CoA carboxy	probable permease,	GTP-binding regula	nu chain	protein -	protein -	ipsilon cha
SUMMARIES	a	136948	EHHU	EHRT	168730	168726	EHMS	538864	837909	T19571	S42659	T02921	T06161	T02235	T02599	FPMS	A03859	A75171	T48197	S28115	JQ1122	T08243	S60266	T02750	D97096	T06814	A46532	S15566	S18738	843147
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	Match Length	426	428	429	107	107	388	548	116	394	1306				1756	605	106	195	539	381	382	382	684	1685	367	384	454	928	1161	110
% Query	Match	62.4	60.3	58.2	41.1	41.1	41.1	41.1	38.3	38.3	38.3	œ	œ	œ	ဖ	o	9	36.2	S	35.1	S	35.1	34.8	٠	•	34.0	•	34.0	•	33.3
	Score	88						58						54	S	51.5	51	51	LO.	49.5			49	49	48	48	48	48	48	47
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hypothetical prote	molybdenum transpo	probable GTP-bindi	GTP-binding regula	protein T6D22.14 [acetyl-CoA carboxy	probable phosphoes	conserved hypothet	hypothetical prote	hypothetical prote	MHC class II E-bet	H-2 class II histo	class II histocomp	probable membrane	Iq heavy chain pre	pyruvate synthase
C86148	AE0595	T16971	RGTOOA	D86215	T09538	C97419	AD2637	T48376	B71044	155951	A60497	S10989	T34940	S04845	A64367
7	7	~	1	~	N		~	~	~	7	N	~	N	~	-
320	352	372	384	2254	2257	242	242	248	198	245	264	264	382	549	270
33.3	33,3	33.3	33.3	33.3	33.3	33.0	33.0	33.0	32.6	32.6	32.6	32.6	32.6	32.6	32.3
47	47	47	47	47	47	46.5	46.5	46.5	46	46	46	46	46	46	45.5

ALIGNMENTS

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                                                                                                                         Query Match 62.4%; Score 88; DB 2; Length 426; Best Local Similarity 69.6%; Pred. No. 4.7e-05; Matches 16; Conservative 2; Mismatches 5; Indels
136948
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292 GETYQCRVTHPHLPRALVRSTTK 314 2 GETYYSRVTHPHLPKDIVRSIAK 24 ò qq

Ignorian chain C region - human C Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999 C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; R:Flanagan, J.G.; Rabbitts, T.H. BMBO J. 1, 655-660, 1982 A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region g A;Reference number: A22771; MUID: 84236029 A:Accession: A22771 MID: 84236029 A:Accession: A22771 A:Accession: A:Accessio

A;Molecule type: DNA A;Residues: 2-428 <UED> A;Cross-references: GB:J00222; NID:9184755

Mon Aug

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A;Cross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:g263169
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Matches 15; Conserv
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                                                                                                                                                                         A; Accession: A46536
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Ayîttle: Purification and characterization of a recombinant human IgE Fc-epsilon fragmen A; Accession: S02438; MUID:88083554

A, Accession: S02438; MUID:88083554

A, Status: nucleic acid sequence not shown
A, Molecule type: mRNA
A, Residues: 98-35 Circ>
R; Zhang, K; Wax, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994

A, Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces A; Recence number: A53116; MUID:94103254

A, Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces A; Retence number: A53116; MUID:94103254

A, Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces A; Retence number: A53116

A, Accession: A3116

A, Molecule type: mRNA
A, Residues: 330-428 czHz>
A; Repsidues: 330-438 czHz>
A; Reference number: A46356; MUID:93122085

A, Retaus: prefluminary
A, Molecule type: mRNA
A, Recision: C4636
A, Reference number: A46356; MUID:93122085
A, Reference number: A46356; MUID:93122085
A, Rocession: C4636
A, Reterences: GB:S55273; NID:9263166; PIDN:AAB24857.1; PID:9263167
A, Recession: D46536
A, Residues: 382-391 cherz>
A, Residues
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A. Molecule type: DNA
A. Recession: A90824
A. Molecule type: DNA
A. Recession: A90824
A. Molecule type: DNA
A. References: GB:J00222; NID:9184755
A: Note: this sequence difference may be due to polymorphism
B. Benitch, H.H.; Johannsson, S.G.O.; Von Bahr-Lindstrom, H.
In Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A. Reference number: A34418
A. Molecule type: protein
A. Residues: 'GAMTU', 6' X', 8-16, 'B', 18-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 12
A. Experimental source: myeloma protein Nd
B. Residues: 'GAMTU', 6' X', 8-16, 'B', 18-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 12
A. Experimental source: myeloma protein Nd
B. Residues: 'GAMTU', 6' X', 8-16, 'B', 18-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 12
A. Experimental source: myeloma protein Nd
B. Residues: 'GAMTU', 6' X', 8-16, 'B', 18-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 12
A. Experimental source: myeloma protein Nd
B. R. Residues: 'GAMTU', 6' X', 9-16, 'B', 18-43, 'B', 18-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 12
A. A. Crossion: B93933; MUID:83065234
A. Molecule type: mRNA
A. Residues: 1-40; 68-114,427-428
A. Molecule type: mRNA
A. Residues: GB:L00022; NID:9185035
B. Ett. 224, 306-310, 1987
A. Molecule type: mRNA
A. Residues: GB:L00022; NID:9185035
B. Ett. 224, 306-310, 1987
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Residues: GB:L00022; NID:9185035
B. Ett. 224, 306-310, 1987
                                                                                                                                                                                                                                                        A.Wolecule type: DNA

A.Kesidues: 320-428 <2HA>

A.Kresidues: 320-428 <2HA>

A.Cross-references: EMBL:X63693; GB:S38668; NID:g32987

R.Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sugi

Wucletc Acids Res. 11, 719-726, 1983

A.Title: Wolecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha

A.Reference number: A93491; WUID:83168897
                                                                                    A;Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A;Reference number: PH1214; MUID:92308839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A93491
A; Molecule type: mRNA
A; Residues: 1-428 CSENA
A; Residues: 1-428 CSENA
A; Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
R; Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A; Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A; Reference number: A90824; MUID:83001945
Zhang, K.; Saxon, A.; Max, E.E.
Exp. Med. 176, 233-243, 1992
Title: Two unusual forms of hume
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A; Gene: GDB:1GHE
A; Cross-references: GDB:119335; OMIM:147180
A; Map position: 14432.33
A; Mathematical Manuroglobulin heterotetramer subunit consists of two identical light (c; Gomplex: An immunoglobulin heterotetramer subunit consists of two identical light (c; Superfamily: immunoglobulin C region; immunoglobulin homology c; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology cimical manuroglobulin homology cimical manurog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin c region; immunoglobulin subunits associate into C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;19-80/Domain: immunoglobulin homology <IMI>
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A;Contents: myeloma IR162
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F:223-291/Domain: Immunoglobulin homology <IM3>
F:227-398/Domain: Immunoglobulin homology <IM3>
F:457-398/Domain: Immunoglobulin homology <IM3
F:46,99,170,240,265,369,413/Binding site: carbohydrate (Asn) (covalent) #status predi
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C.Jace-1982 #text_change 16-Jul-1999
C.Jaces-17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C.Jacession: A93442; A90937; A03143
R.Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A.;Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
A.;Reference number: A93442; MUID:83064537
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                                                                                                                                                       A) Status: preliminary; not compared with conceptual translation A, Status: DNA A, Molecule type: DNA A, Residues: 401-428 <HE3> A; Cross-references: GB:S53497; NID:g263162; PIDN:AAB24855.1; PID:g263163 A; Cross-references: B cell myeloma U-266 A; Note: sequence extracted from NCBI backbone (NCBIP:123483) C; Genetics:
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A; Residues: 1-429 <HEL>
A; Experimental source: strain LOU/c/Wsl, immunocytoma IR2
B; Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
BNA 1, 335-343, 1982
                                                          A;Note: sequence extracted from NCBI backbone (NCBIP:125299)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 85; DB 1; Ler
Pred. No. 0.00013;
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Pred. No. 0.00036;
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65.2%; Pred. No. v...
3; Mismatches
A; Experimental source: B cell myeloma U-266
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A; Residues: 'N', 169-307,'L', 309-342 <KIN>
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C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (A.C.Superfamily: immunoglobulin C. region; immunoglobulin homology immunoglobulin (C.Superfamily: immunoglobulin homology (Fragment) and the consist of the 
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hypothetical protein YKL084w - yeast (Saccharomyces cerevisiae)

c; Species: Saccharomyces cerevisiae

c; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 29-Oct-1999

C; Accession: S37909

R; Pohl, T.M.; Pohl, F.M.

Submitted to the Protein Sequence Database, March 1994

A; Reference number: S37897

A; Accession: S37909

A; Residues: 1-116 < Pohl>
A; Residues: 1-116 < Pohl>
A; Estiques: 1-116 < Pohl>
A; Estiques: 1-116 < Pohl>
A; Cross-references: EMBL: 228084; NID: 9486122; PID: 9486123; GSPDB: GN00011; MIPS: YKL084

A; Experimental source: strain S288C

G; Genetics: A; Genetics: A; Genetics: 11L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kipp, B.; Becker, W.; Schlaak, M. submitted to the EMBL. Data Library, November 1993 submitted to the EMBL. Data Library, November 1993 A;Description: Combination of a defined specificity and desired isotype by cloning of A;Reference number: S38864
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C;Species: Wus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C;Accession: S38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:227397; NID:9416537; PIDN:CAA81788.1; PID:9940782
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;353-421/Domain: immunoglobulin homology <IMM>
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Pred. No. 1.1;
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Pred. No. 1;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 GYGYOCIVDHPDFPKPIVRSITK 269
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Best Local Similarity 56.5%;
Matches 13; Conservative
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Best Local Similarity 56.5%;
Matches 13; Conservative
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52.68;
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Best Local Similarity
                                                                                                             1-388 <LIU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-548 <KIP>
                                                                            A; Molecule type: mRNA
A; Residues: 1-388 <LII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                           A; Accession: A02144
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                                                                                                                                                                                                                                                                                                                                                 ige chain C3 region - mouse (fragment)
(5.5pectes: Mus musculus (house mouse)
(5.5pectes: Mus musculus (house mouse)
(5.5pectes: Nus musculus (house mouse)
(5.5pectes: 01-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
(5.Accession: 168730 Makauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid
A;Reference number: 154443; MUID:88152907
A;Accession: 168730
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ignoration control region - mouse (fragment)
(5)Species: Mus musculus (house mouse)
(5)Species: Mus musculus (house mouse)
(5)Species: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
(5)Accession: 168726
(8)Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
(8)Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
(8)A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid
(8)Reference number: 154443; MUID:88152907
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R; Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
A; Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA. A; Reference number: A02144; MUID:83117774
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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A; Residues: 1-107 <RES>
A; Cross-references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460
C; Superfamily: Immunoglobulin C region; immunoglobulin homology
F; 22-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-107 <RES>
A; Cross-references: GB:M22933; NID:g194464; PIDN:AAA37915.1; PID:g194469
C; Superfamily: Lmmunoglobulin C region; immunoglobulin homology
F; 22-90/Domain: immunoglobulin homology <IMM>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.1%; Score 58; DB 2; ilarity 56.5%; Pred. No. 0.27; Conservative 0; Mismatches
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                                        Mismatches
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                                                                                                                                              284 GEGYQCRVDHPFPKPIVRSITK 306
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Matches 13; Conserv
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Best Local Similarity
Matches 13; Conserv
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Score 54; DB 2
Pred. No. 18;
3; Mismatches
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55.6%;
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Best Local Similarity
Matches 10; Conserv
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A; Residues: 1-1306 <ASSH>
A; Cross-references: EMBL:224449
C; Function:
A: Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
A; Pathway: fatty acid biosynthesis
C; Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-
C; Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acetyl-CoA carboxylase (EC 6.4.1.2) - maize (fragment)
C.Species: Zea mays (maize)
C.Species: Zea mays (maize)
C.Date: 07-Sep-1994 #sequence_revision 24-oct-1998 #text_change 17-Mar-1999
C.Accession: S42659, S34639,
Maitfield, P.R.,
Plant Mol. Biol. 24, 35-49, 1994
A.Fille: Molecular cloning of two different cDNAs for maize acetyl CoA carboxylase.
A.Reference number: S42659, MuID:94154242
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                                                                                                                                                                       C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19571
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Accession: T02921
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Pred. No. 14; 
3; Mismatches 5; Indels
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A;Introns: 32/3; 72/3; 117/1; 164/3; 193/3; 247/1; 335/3; 363/3
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     Indels
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   7;
                                                                                                                                                          hypothetical protein C29F7.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-394 <MIL>
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Pred. No. 4;
     Mismatches
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submitted to the EMBL Data Library, March 1997
Reference number: 219144
A;Accession: T19571
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55.6%;
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                                    7 SRVTHPHLPKDIVRSIAKC
     Conservative
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Best Local Similarity 55.6
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity es 9; Conserv
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A;Gene: CESP:C29F7.1
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Matches 9
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N; Alternate names: acetyl-coenzyme A carboxylase C; Species: Triticum aestivum (common wheat) C; Accession: Trollo1; Trollo2; Sq2660; S78600; S35559 C; Accession: Trollo1; Trollo2; Sq2660; S78600; S35559 R; Gornicki, P.; Faris, J.; Podkowinski, J.; Gill, B.; Haselkorn, R. Proc. Natl. Acad. Sci. U.S.A. 94, 14179-14184, 1997 A; Title: Plastid localized acetyl-CoA carboxylase of bread wheat is encoded by a sing A; Accession: T06161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: S4260
A, Molecule type: mRNA
A; Residues: 'WarYM',1711-2026,'K',2028-2073,'F',2075-2108,'V',2110-2120,'L',2122,'A',
A; Cross-references: EMBL:223038; NID:9396278; PIDN:CAA80573.1; PID:9396279
A; Accession: S78600
A; Molecule type: protein
A; Residues: 1847-1852,'E',1854-1863;1947-1962,'D',1964;2085-2091,'HL';2139-2155,'I',2
C; Genetics:
A; Genetics:
A; Genetics:
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C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biot
C;Reywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule Lype: DNA
A; Residues: 1-10, Fr. 12-67, Hr, 69-502, Tr, 504-619 CGOR2>
A; Cross-references: EMBL:AF029897; NID:92827153; PIDN:AAC39332.1; PID:92827154
A; Experimental source: cv. Hard Red Winter Tam 107, 11ght-grown seedling
R; Elborough, K.M.; Simon, J.W.; Swinhoe, R.; Ashton, A.R.; Slabas, A.R.
Plant Mol. Biol. 24, 21-34, 1194
A; Title: Studies on wheat acetyl COA carboxylase and the cloning of a partial cDNA.
A; Reference number: S42660; MUID:94154234
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Notecule type: mRNA
A;Residues: 1-2311 GGOR1A
A;Cross-references: EMBL:AF029895; NID:92827149; PIDN:AAC39330.1; PID:92827150
A;Experimental source: cv. Hard Red Winter Tam 107, light-grown seedlings
A;Accession: T06162
A;Status: preliminary; translated from GB/EMBL/DDBJ
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acetyl-CoA carboxylase (EC 6.4.1.2) - wheat
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A. Molecule type: mRNA
A. Residues: 1-597, E', 599-605 <LAW>
A. Residues: 1-597, E', 599-605 <LAW>
A. Crossreferences: GB: WOU743
B. Minghetti, P.P.; Law, S.W.; Dugaiczyk, A.
B. Mol. Biol. Evol. 2, 347-358, 1985
Mol. Biol. Evol. 2, 347-358, 1985
Mol. Biol. Evol. 2, 347-358, MUD: 88216123
A. Title: The rate of molecular evolution of alpha-fetoprotein approaches that of pseu A. M. Contents: annotation; revision to residue 598
A. Contents: annotation; revision to residue 598
A. M. M. B.; Cooper, D. L.; Eiference A93254 as Glu, should have been reported a R. Gorin, M. B.; Cooper, D. L.; Eiference, P. V. Van de Rijn, P.; Tilghman, S.M.
J. Biol. Chem. 256, 1954-1959, 1981
A. Title: The evolution of alpha-fetoprotein and albumin: I. A comparison of the prima A. Reference number: A92305; MUID: 81117287
A. Accession: A92305
A;Gene: At2g14770; F26C24.9
A;Map position: 2
A;Introns: 42/1; 351/3; 418/1; 617/3; 659/3; 690/3; 725/1; 758/3; 778/3; 812/3; 902/2
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C. Keywords: embryo; fetus; globulin; glycoprotein; metal binding; plasma
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-60/Pomain: serum albumin repeat homology <SA1>
F;20-198/Domain: serum albumin repeat homology <SA2>
F;20-198/Domain: serum albumin repeat homology <SA2>
F;20-58/Domain: serum albumin repeat homology <SA3>
F;20-58/Domain: serum albumin repeat homology <SA3>
F;20/Binding site: copper (His) #status predicted
F;25-110,109-120,144-189,188-197,220-266,265-273,285-299,298-309,380-389,412-458,457-F;247,498/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Contents: annotation; exon-intron junctions
C;Conment: Mouse AFP has two carbohydrate chains and was found to bind estrogens and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Homology between the primary structure of alpha-fetoprotein, deduced from a A;Reference number: A93254; MUID:81197641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-fetoprotein precursor - mouse
N;Alternate names: AFP; alpha-1-fetoprotein precursor; alpha-fetoglobulin precursor C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 01-Sep-1981 #sequence_revision 28-May-1986 #text_change 12-Jun-1998
C;Accession: A93254; A92305; A03235
R;Law, S.W.; Dugaiczyk, A.
Nature 291, 201-205, 1981
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A;Residues: 15-532, 'RAKL', 538-605 <GOR>
A;Cross-references: GB:M16381
A;Note: the beginning of the mature protein was placed at residue
R;Eiferman, F.A.; Young, P.R.; Scott, R.W.; Tilghman, S.M.
Nature 294, 713-718, 1981
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Pred. No. 38;
6; Mismatches
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57.9%; Pred. No. 15;
Live 3; Mismatches
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                                                                                                                                                                  36.9%;
llarity 37.5%;
Conservative
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354 YSR-THPNLPVSVILRIAK 371
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Best Local Similarity 57.9
Matches 11; Conservative
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Best Local Similarity
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R; Egli, M.A.; Lutz, S.M.; Somers, D.A.; Gengenbach, B.G.
Palatt Physiol. 108, 1299-1300, 1995
A; T1tle: A malze acctyl-coenzyme A carboxylase CDNA sequence.
A; Reference number: Z14632; MUID:95357420
A; Accession: T02235
A; Accession: T02235
A; Accession: T02235
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-2325 < EGL>
A; Cross-references: EMBL:019183; NID:91045304; PIDN:AAA80214.1; PID:9854731
A; Residues: 1-2325 < EGL>
A; Cross-references: EMBL:019183; NID:91045304; PIDN:AAA80214.1; PID:9854731
A; Experimental source: strain A188; leaf
C; Function:
A; Description: catalyzes the ATP-dependent carboxylation of acctyl-CoA to malonyl-CoA A; Pathway: fatty acid biosynthesis
C; Superfamily: human acctyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C; Keywords: ligase
F; 134-640/Domain: biotin carboxylase homology < ELPB>
F; 767-839/Domain: lipoyl/biotin-binding homology < LPB>
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujli, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
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R; Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998
A; Description: Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence.
A; Reference number: 214680
A; Accession: T02599
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A;Accession: C84521
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A;Residues: 1-1756 <STO>
A;Cross-references: GB:AE002093; NID:g3252818; PIDN:AAC24188.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: acetyl-coenzyme A carboxylase
C;Species: Zea mays (maize)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jan-2000
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A;Molecule type: DNA
A;Residues: 1-1756 <ROU>
A;Cross-references: EMBL.AC004705; NID:93252804; PID:93252818
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Pred. No. 26;
3; Mismatches
   ore 54; DB 2
ed. No. 26;
Mismatches
   Score 54;
Pred. No.
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55.6%;
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38.38;
55.68;
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                                                                    Conservative
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Best Local Similarity 55.6
Matches 10; Conservative
Query Match
Best Local Similarity
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pyrococcus
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  drosophila
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Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;

(In) Bach M.K. (eds.).

Immediate hypersensitivity: modern concepts and developments, pp.1-36, Marcel Dekker, New York (1978).
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MEDILINE-8318089; PubMed-6300763;
MEDILINE-8318089; PubMed-6300763;
Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,
Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
"Modecular cloning and nucleotide sequencing of human immunoglobulin
epsilon chain cDNA";
Nucleic Acids Res. 11:719-726(1983).
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Catarrhini; Hominidae; Homo.
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MEDLINE-84207910; PubMed-6327276;
Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;
"Long terminal repeat-like elements flank a human immunoglobulin
                                         09v198
002484
09p107
P02773
053210
P73293
P73293
084457
P01877
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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EMBO J. 1:1539-1544(1982).
                                         RPOD_PYRAB
YIE2_HSVB4
SYM_CHLMU
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RPOL_KLULA
Y4UH_RHISN
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CDSA_CHLTR
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MEDLINE=84236029; Pubmed=6234164;
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Mammalia, Eutheria, Primates,
NCBI_TaxID=9606,
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EMBO J. 1:655-660(1982).
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EPC_HUMAN
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P02772
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083491
                                            Compugen Ltd
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                            August 26, 2002, 10:17:02;
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1 CGETYYSRVTHPHLPKDIVRSIAKC
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WVC_PSEFL
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UNC_RICENIA
UVC_RICENIA
IRSI_RAT
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CAH1_MOUSE
Y760_METJA
TPS2_MOUSE
MUCB_HUMAN
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YK14_YEAST
FETA_MOUSE
Y116_ADE02
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POL_SFV1
GBA1_LYCES
BAR1_HUMAN
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GVC1_HALN1
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Total number of

Searched:

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Database :

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OM protein

Run on:

Scoring table:

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'Structure and evolution of the heavy chain from rat immunoglobulin
                     Nucleic Acids Res. 10:6041-6049(1982)
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
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SMART; SM00410; IG_like; 3.
SMART; SM00407; IGcl; 1.
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Best Local Similarity
Matches 16; Conserv
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REVISIONS.
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P01855;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-Box norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa Chordata; Craniata; Vertebrata; Euteleostomi;
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*STRAIN-LOU/C/W37;
*MEDLINE-83064537; PubMed=6292865;
Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
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                                                                                                                                                                                                                                       Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                                                     INTERCHAIN (WITH A LIGHT CHAIN)
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         Padlan E.A., Davies D.R.; "A model of the F-C- of immunoglobulin E."; Submitted (JUL-1993) to the PDB data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                      POLYMORPHISM
                                                                                                                            EMBL; 100022; AAB59424.1; ALT_INIT
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W.
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SMART; SM00407; IGc1; 4.
PROSITE; PS00290; IG_MHC; 3.
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InterPro; IPR003597; Ig_cl.
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PIR; A22771; A22771.
PIR; A23195; A23195.
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SEQUENCE OF 205-306 FROM N.A.
MEDLINE-82174576: PubMed-6803238;
Hellman L., Pettersson U., Bennich H.;
Characterization and molecular cloning of the mRNA for the heavy (epsilon) chain of rat immunoglobulin E ";
Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                      MEDLINE-83182019; PubMed-6820340;
Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
construction, identification, and DNA sequence.";
DNA 1:335-343(1982).
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Pred. No. 9.6e-05;
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P -> L (IN REF. 2).
D2970B34EF8A72B0 CRC64;
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Immunoglobulin domain; Immunoglobulin C region.
SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
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MEDLINE=81197641; PubMed=6164927;
Law S.W., Dugaiczyk A.;
Homology between the primary structure of alpha-fetoprotein, deduced from a complete CDNA sequence, and serum albumin.";
Nature 291:201-205(1981).
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"The rate of molecular evolution of alpha-fetoprotein approaches that
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 1; Length 116;
Pred. No. 0.34;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-UUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-
                                 SECUENCE FROM N.A.
Pohl T.M., Pohl F.M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEOUENCE 116 AA; 13641 MW; 57464E5FD9A591F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eiferman F.A., Young P.R., Scott R.W., Tilghman S.M.; "Intragentc amplification and divergence in the mouse alpha-fetcprotein gene."; Nature 2947:713-718(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Liver;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88216123; PubMed-2452956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=82103990; Pubmed=6172714;
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52.6%;
                                                                                                                                                                                                                                            EMBL; Z28084; CAA81922.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 SRCVHWHLPKDVIAIRFKC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 SRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                   PIR; S37909; S37909.
SGD; S0001567; YKL084W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fetoprotein).
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P02772;
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                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                               SEQUENCE OF 34-421 FROM N.A.
MEDLINE-83117774; PubMed-6818553;
Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
"Cloning and nucleotide sequence of mouse immunoglobulin epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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(POTENTIAL).
(POTENTIAL).
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Hypothetical 13.6 kDa protein in MDH1-VMAS intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.1%; Score 58; DB 1; Length 421; 56.5%; Pred. No. 0.34;
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               Submitted (APR-1986) to the EMBL/GenBank/DDBJ databases.
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CH3.
CH4
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHAPTER GLONG.
N-LINKED GLONG.
                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003600; Ig_like.
Pfam; PF00047; ig; 4.
SMART; SM00410; IG_like; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GETYYSRVTHPHLPKDIVRSIAK 24
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                                                                                                                                                                                                                                                                                                                                                          EMBL; X01857; CAA25978.1; -.
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PIR; A02144; EHMS.
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415
421 AA;
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Matches 13; Conserv
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198
305
23
121
226
330
                                                                                                        "Cloning and
chain cDNA.";
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P36078;
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DISULFID
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YKI4_YEAST

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MW.
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                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                       605 AA;
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SEQUENCE 10
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P03287;
                                                     DISULFID
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Y116_ADE02
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Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fuehl P., Lewis S., Martsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake U., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Ming B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Maynshaw, Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                     SEQUENCE OF 15-605 FROM N.A.
MEDLINE-81117287; PubMed=6161929;
GOLIN M.B., Cooper D.L., Elferman F.A., van de Rijn P., Tilghman S.M.;
"The evolution of alpha-fetoprotein and albumin. I. A comparison of the primary amino acid sequences of mammalian alpha-fetoprotein and
                                                                                                                                                        Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00212; ALBUMIN; 2.
Glycoprotein; Sulfation; Albumin; Plasma; Embryo; Repeat;
Metal-binding; Signal.
                                                                                                                                                                                                                                                                         J. BIOL. Chem. 256:1954-1959(1981).
-- FUNCTION: BINDS ESTROGENS, FATTY ACIDS AND METALS.
-- SUBCELLULAR LOCATION: Extracellular.
-- TISSUE SPECIFICITY: PLASMA.
-- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-- PTM: GLYCOSTRATED: HAS TWO CARBOHYDRATE CHAINS.
-- PTM: GLYCOSTRATED (BY SIMILARITY).
-- PTM: SULFATED (BY SIMILARITY).
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ALPHA-FETOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A03235; FPMS.
HSSP; P02768; 1BJ5.
MGD; MGI:87951; Afp.
InterPro; IPR000264; Serum_albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00273; transport prot; 3. PRINTS; PR00802; SERUMALBUMIN. ProDom; PD002486; Serum_albumin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M16389; AAA37189.1; JOINED.
M16390; AAA37189.1; JOINED.
M16391; AAA37189.1; JOINED.
M16392; AAAA37189.1; JOINED.
M16393; AAAA37189.1; JOINED.
M16393; AAA37189.1; JOINED.
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                                                                                                                                                                                Nature 409:685-690(2001).
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605
198
390
588
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M16387;
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REPEAT
CARBOHYD
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human adenovirus type 2. Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.NCBI_TaxID=10515;
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(POTENTIAL)
                              (POTENTIAL)
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CE09E9F50D74619A CRC64;
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106 AA; 11668 MW; 12692EF62B02E3A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.2%; Score 51; DB 1;
llarity 62.5%; Pred. No. 0.87;
Conservative 1; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
Hypothetical 11.6 kDa early protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51.5; DB
Pred. No. 4.5;
3; Mismatches
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Best Local Similarity
Matches 10; Conserv
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Halobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GROWTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
                                                                                                                                                                                                                                        J. MOI. BIOJ. 227:586-592(1992).
-I- FUNCTION: MAY COMFER STABILITY TO THE GAS VESICLE MEMBRANES. GAS VESICLES ARE SMALL, HOLLOW, GAS FILLED PROTEIN STRUCTURES THAT ARE FOUND IN SEVERAL PROKARYOTIC PLANKTONIC MICROORGANISMS. THEY ALLOW THE POSITIONING OF THE BACTERIA, AT THE FAVORABLE DEPTH FOR
                                                                                                                                                   Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloferax.
NCBI_raxID=2252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                          in
                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: BINDS TO THE EXTERNAL SURFACE OF THE GAS
                                                                                                                                                                                          STRAIN-DSM 1411;
MEDLINE-93021102; PubMed=1404376;
MEDLINE-93021102; PubMed=1404376;
MEDLINE C., Krueger K., Offner S., Pfeifer F.;
"Three different but related gene clusters encoding gas vesicles halophilic archaea.";
                                                                                                                                                                                                                                                                                                                 SIMILARITY: VERY DISTANT, TO GAS VESICLE PROTEINS TYPE C OF CYANOBACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASP/GLU-RICH (ACIDIC).
9FB48199D0305921 CRC64;
                                                                                                                                             Halobacterium mediterranei (Haloferax mediterranei)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                          JUL-1993 (Rel. 26, Created)
JUL-1993 (Rel. 26, Last sequence update)
JUL-1998 (Rel. 36, Last annotation update)
vesicle protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49.5; DB
                                                                          381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 5.5;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVC1_HALN1 STANDARD; P24574; Q9H117; 01-MAR-1992 (Rel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42653 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.1%;
64.3%;
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                      23 YSRATHRHSGKTVVRS 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
        6 YSRVTHPHLPKDIVRS 21
                                                                           STANDARD;
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343 CGE-YYQAITEPHL 355
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                                                                                                                                                                                                                                                                                                              VESICLE MEMBRANE.
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123
161
193
233
246
381 AA;
                                                                                                                                                                                  FROM N.A.
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gas vesicle;
                                                                                             01-JUL-1993
                                                                                                     01-JUL-1993
15-JUL-1998
                                                                         GVPC_HALME
Q02228;
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SEQUENCE
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MEDLINE-20504483; PubMed-1010595);

NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

"Genome sequence of Halobacterium species NRC-1.";

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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J. Mol. Biol. 227:586-592(1992).
J. Mol. Biol. 227:586-592(1992).
-!- FUNCTION: MAY CONFER STABILITY TO THE GAS VESICLE MEMBRANES. GAS VESICLES ARE SMALL, HOLLOW, GAS FILLED PROTEIN STRUCTURES THAT ARE FOUND IN SEYERAL PROKARYOTIC PLANKTONIC MICROORGANISMS. THEY ALLOW THE POSITIONING OF THE BACTERIA, AT THE FAVORABLE DEPTH FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=NRC-1; PLASMID=DNRC100;
MEDLINE=99063795; Pubmed=9847077;
NG W.V., Cluifo S.A., Smith T.M., Bungarner R.E., Baskin D., Faust J.,
Hall B., Loretz C., Seto J., Slagel J., Hood L., DasSarma S.;
Snapshot of a large dynamic replicon in a halophilic archaeon:
megaplasmid or minichromosome?";
Genome Res. 8:1131-1141(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NRC-817; PLASMID=PHH1;
MEDLINE=92065812; PubMed=1956294;
Horne M., Englert C., Wimmer C., Pfeifer F.;
"A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis in halophilic archaebacteria.";
Mol. Microbiol. 5:1159-1174(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Englert C., Krueger K., Offner S., Pfeifer F.; "Three different but related gene clusters encoding gas vesicles in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-NRC-1; PLASMID-PNRC100; STRAIN-NRC-1; PLASMID-PNRC100; MEDLINE-91323716; PubMed-1864501; Jones J.G., Young D.C., Dassarma S.; Structure and organization of the gas vesicle gene cluster on the Halobacterium halobium plasmid pNRC100.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: BINDS TO THE EXTERNAL SURFACE OF THE GAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VESICLE MEMBRANE.
SIMILARITY: VERY DISTANT, TO GAS VESICLE PROTEINS TYPE C OF
                                                                                                                                                                            Halobacterium sp. (strain NRC-1), and Halobacterium sp. (strain NRC-81). Plasmid pNRC100, Plasmid pNRC200, and Plasmid pHH1. Archaea; Buryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                               (GVPC1 OR GVPC OR VNG5032G) AND (GVPC2 OR VNG6031G)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gas vesicle protein C 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NRC-817; PLASMID=pHH1; MEDLINE=93021102; PubMed=1404376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-NRC-1; PLASMID-pNRC200;
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=64091, 148370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 102:117-122(1991)
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NP_BIND
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                                                                                                                                                    g
                                                                                                                                                                                                                        SIGNALING SYSTEMS.
-!- SUBUNT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
-!- SUBUNT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
-!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 2 (G(S)).
                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RWBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@labs.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pisum sativum (Garden pea).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-CV. ALASKA; TISSUE-Apical bud;
Marsh J.F., Kaufman L.S.;
Marsh J.F., Kaufman L.S.;
Marsh J.F., Kaufman L.S.;
Marsh J.F. (APR-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: GUANINE NUCLECTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLTED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanine nucleotide-binding protein alpha-2 subunit (GP-alpha-2).
GPA2 OR GA2.
                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                  Score 49.5; DB 1; Length 382;
Pred. No. 5.5;
1; Mismatches 3; Indels
                                                                                                                  Complete proteome.
7 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                       ASP/GLU-RICH (ACIDIC).
171DBEB4C0364F46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              384 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00275; G-alpha; 1.
GTP-binding; Transducer; ADP-ribosylation.
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001019; Gprotein_alpha. Pfam; PF00503; G-alpha; 1.
                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                               EMBL; AF016485; AAC82810.1; --
EMBL; AC00142; AAC8027.1; --
EMBL; X57161; CAA40451.1; --
EMBL; X64729; CAA45981.1; --
PIR; J01122; J01122.
PIR; J2483; S12483.
PIR; S28128; S28128; Com
Gas vesicle; Plasmid; Repeat; Com
                                                                                                                                                                                                                                   42391 MW;
                     EMBL; M58557; AAA98197.1; -.
                                                                                                                                                                                                                                                                  35.1%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U97044; AAB57826.1; -
                                                                                                                                                                                                                                                                              Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                             344 CGE-YYQAITEPHL 356
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004279;
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REPEAT
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MEDLINE-90080148; PubMed=2152825;
MEDGIAE-90080148; PubMed=2152825;
Mergla A., Shaw K.E.S., Lackner J.E., Luciw P.A.;
Relationship of the env genes and the endonuclease domain of the polgenes of similar foamy virus type 1 and human foamy virus.";
J. Virol. 64:406-410(1990).
III. PTW: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
III. SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A9.
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE-91276270; PubMed-1647358;
MEDILINE-7.., Kay A., Hayat M., Ravier R., Peries J., Gallbert F.;
"Sequence analysis of the simlan foamy virus type 1 genome.";
Gene 101:185-194(1991).
                          GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

ADP-RIBOSYL[1] (BY ACTION OF CTX).

6B0963393FD20BA4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
POL polyprotein [Contains: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease].
                                                                                                                                                                                                Score 48; DB 1; Length 384; Pred. No. 9.2;
                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mergia A., Luciw P.A.; "Replication and regulation of primate foamy viruses."; Virology 184:475-482(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simian foamy virus (type 1) (SFV-1).
Viruses; Retroid viruses; Retroviridae; Spumavirus.
NCBI_TaxID=11964;
GTP (BY SIMILARITY)
GTP (BY SIMILARITY)
GTP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1161 AA
                                                                                                                                                                                                                                                        4; Mismatches
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EMBL; X58464; CAA41394.1; -.
EMBL; M33561; AAA47793.1; -.
PIR; A33562; A33562.
PIR; S15566; S15566.
PIR; S18738; S18738.
HSSP; P03355; 1MML.
MEROPS; A09.001; -.
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InterPro; IPR001584; Rve.
InterPro; IPR001641; Spuma_A9PTase.
Pfam; PF00075; rnaseH; 1.
Pfam; PF00665; rve; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-970 FROM N.A. MEDLINE-91361538; Pubmed-1653483;
                                                                                                                44669 MW:
                                                                                                                                                                                                34.0%;
50.0%;
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|125 SRLDYPHLTKDLAKEI 140
                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                7 SRVTHPHLPKDIVRSI 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
46
219
288
191
384 AA;
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POL_SFV1
P23074;
01-NOV-1991 (
01-JUL-1993 (
16-OCT-2001 (
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Gaps

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Indels

3;

d. No. 13; Mismatches

Pred.

53.3%;

Conservative

Similarity 8; Conserv

Best Local Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNALING SYSTEMS.
-!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
-!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 2 (G(S)).
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eŭkaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Pagermatophyta; Pagermatophyta; Core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum. NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last annotation update)
Guanine nucleotide-binding protein alpha-1 subunit (GP-alpha-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

ADP-RIBOSYL[1] (BY ACTION OF CTX).

SC95ED74EFC01A0A CRC64;
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            PRINTS; PR00920; SPUMVIRPTASE.
Transferase; RNA-directed DNA polymerase; Hydrolase; Nuclease;
                                                                                                                                                              Length 1161;
                                                                                                                                                                                            Indels
                                                                                                                   08D09D1D6BB4C14C CRC64;
                                         Endonuclease; Aspartyl protease; Polyprotein.

ACT_SITE 36 36 BY SIMILARITY.

CONFLICT 236 236 T -> I (IN REF. 2).

CONFLICT 910 910 S -> G (IN REF. 2).

CONFLICT 950 950 A -> T (IN REF. 2).

SEQUENCE 1161 AA; 131717 WW; 08D09D1D6BB4C14C
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                                                                                                                                                              DB 1;
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PIR; JH0514; RGTOOA.
HSSP, PO10124; 1AS3.
InterPro; IPR001019; Gprotein_alpha.
Pfam; PF00503; G-alpha; 1.
PRINTS; PR00318; GPROTEINA.
SMARY; SN00275; G-alpha; 1.
GTP-binding; Transducer; ADP-ribosylation.
                                                                                                                                                                                                                                                                                                                           384 AA
                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                          34.0%; Score 48; DB 47.4%; Pred. No. 29; iive 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                      (Rel. 23, Created)
(Rel. 23, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44903 MW;
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                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                      7 SRVTHPHLPKDIVRSIAKC
                                                                                                                                                                                                                                                                                                                           STANDARD;
Pfam; PF00078; rvt; 1
                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (
01-AUG-1992 (
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                GPA1 OR GA1.
                                                                                                                                                                                                                                                                                                                           GBA1_LYCES
P26981;
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MOD_RES
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                                                                                                                                                                                                                                                                                              RESULT 11
GBA1_LYCES
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Matches
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Length 384;

DB 1;

33.3%; Score 47;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 285:1576-1579(1999).

-! FUNCTION: IMPLICATED IN BRCA1-MEDIATED TUMOR SUPPRESSION. MAY, AS PART OF THE RNA POLYMERASE-2 HOLOENZYME, FUNCTION IN THE CELLULAR RESPONSE TO DNA DAMAGE. IN VITRO, INHIBITS PRE-MRNA 3' CLEAVAGE.
-!- SUBUNT: HOWO-AND HETERODIMER. PREFERENTIALLY FORMS HETERODIMERS WITH BRCA1. CAN ALSO PORM HETERODIMERS WITH GSTF-50.
-!- SUBCELLULAR LOCATION: NUCLEAR. DURING S PHAGE OF THE CELL CYCLE, CO-LOCALIZES WITH BRCA1 INTO DISCRETE SUBNUCLEAR FOCI.
-!- PTW. PROCESSED DORING APPOPTOSIS. THE HOWOUNINR IS MORE SUSCEPTIBLE TO PROTEOLYTIC CLEAVAGE THAN THE BARDI/BRCA1 HETERODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANTS.
MEDLINE-98087570; PubMed=9425226;
Thai T.H., Du F., Tsan J.T., Jin Y., Phung A., Spillman M.A.,
Massa H.F., Muller C.Y., NowAching R., Mathis J.M., Miller D.S.,
Trask B.J., Baer R., Bowcok A.M.;
"Mutations in the BRCA1-associated RING domain (BARD1) gene in primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99407028; PubMed-10477523;
Kleiman F.E., Manley J.L.;
"Functional interaction of BRCA1-associated BARD1 with polyadenylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 3 ANK REPEATS.
-!- SIMILARITY: CONTAINS 2 BRCT DOMAINS.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-26 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-9709944; PubMed-8944023; Wu L.C., Wang Z.W., Tsan J.T., Spillman M.A., Phung A., Xu X.L., Yang X.C., Wang Z.W., Tsan J.T., Spillman M.A., Baer R.; Identification of a RING protein that can interact in vivo with the BRCAl gene product.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meza J.E., Brzovic P.S., King M.-C., Klevit R.E.;
"Mapping the functional domains of BRAC1. Interaction of the ring finger domains of BRAC1 and BARD1.";
J. Biol. Chem. 274:5659-5665(1999).
                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                   BARI_HUMAN STANDARD; PRT; 777 AA. 099728; 043574; 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) BRCAl-associated RING domain protein 1 (BARD-1).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast, ovarian and uterine cancers.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hum. Mol. Genet. 7:195-202(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OVARIAN AND UTERINE CANCERS
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nat. Genet. 13:430-440(1996).
                                    126 RLDYPHLTKDLVQDI 140
22
                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
RVTHPHLPKDIVRSI
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264 AA.

STANDARD;

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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                      STRAIN-LEWIS FAMILIARIS; TISSUE-Bone marrow;
MEDLINE-90356406; Pubmed-238888;
Syha-Jedelhauser J., Reske K.;
"Sequence of rat cDNA clone pLR beta 112 coding for the RT1.D beta I
                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
RT1 class II histocompatibility antigen, D-1 beta chain precursor.
                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 18:4598-4598(1990).
-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                     chain."
                                                   P18211
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      and for commercial
                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                   DR InterPro; IPR00135; BRCT.
DR InterPro; IPR00135; BRCT.
DR InterPro; IPR00135; BRCT.
DR Fdan; PF00023; BRCT; 2.
DR Pfan; PF00023; BRCT; 2.
DR PART; SM00248; ANK; 3.
DR SMART; SM00248; ANK; 3.
DR SMART; SM00184; RING; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50099; BRCT; 2.
DR PROSITE; PS50099; ZF_RING_1; 1.
DR PROSITE; PS50099; ZF_RING_1; 1.
DR PROSITE; PS50099; ZF_RING_2; 1.
DR PROSITE; PS50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P -> S (FREQUENT POLYMORPHISM IN CAUCASIANS; LESS FREQUENT IN AFRICANS). FTICH-WARD.010354.

K -> E (UNCLASSIFIED).
/FTICH-WAR_010355.
V -> M (UNCLASSIFIED).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANK 1.
ANK 2.
ANK 2.
ANK 2.
BACT 1.
BRCT 1.
BRCT 2.
REQUIRED FOR INTERACTION WITH BRCA1.
POLY LEU.
POLY LEU.
POLY SER.
      Usage by
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R -> S (IN REF. 2).
Q -> R (IN REF. 2).
modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@lsb-sib.ch).
                                                                          AF038042; AAB999781; AR038042; AR038034; AAB999781; JOINED. AR038035; AAB999781; JOINED. AR038036; AAB999781; JOINED. AR038038; AAB999781; JOINED. AR038039; AAB999781; JOINED. AR038040; AAB999781; JOINED. AR038041; AAB999781; JOINED. AR038041; AAB999781; JOINED. AR038041; AAB999781; JOINED.
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                                                               EMBL; U76638; AAB38316.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153
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                                                                                                                                      EMBL; AF03803
EMBL; AF03803
EMBL; AF03803
EMBL; AF03804
EMBL; AF03804
HSSP; PIS919;
MIM; 601593;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                           RT1 CLASS II HISTOCOMPATIBILITY ANTIGEN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 264;
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EXTRACELLULAR BETA-1.
EXTRACELLULAR BETA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONNECTING PEPTIDE
                                                                                                                                                       EMBL; X53054; CAA37221.1; -
PIR; $10989; $10989;
HSSP; P13760; 2SEB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR00353; MHC_II_beta.
Pfam; PF00045; ig; 1.
ProDom; PD000328; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC II; Transmembrane; 61ycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 1;
Pred. No. 12;
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
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BY SIMILARITY
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29876 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.6%; 47.1%;
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195 GEVYTCQVEHPSLPSPV 211
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Best Local Similarity 47.1
Matches 8; Conservative
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42
144
144
264 AA;
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01-NOV-1995 (
16-OCT-2001 (
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P32966;
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DISULFID
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CARBOHYD
SEQUENCE
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UVRC_PSEFL
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Gaps

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33.3%; Score 47; DB 1; Length 777; 52.6%; Pred. No. 27; 1ve 2; Mismatches 7; Indels

Query Match 33.3 Best Local Similarity 52.6 Matches 10; Conservative

(602 STVTHVVVPGDAVQSTLKC 620

SRVTHPHLPKDIVRSIAKC 25

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                                                                                                                                                                                                                                                                                                                                                                                        synthesis and suppression of black root rot of tobacco.";
Proc. Natl. Acad. Sci. U.S.A. 89:1562-1566(1992).
-!- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT
CATALYZES THE EXCTSION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS
PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). ATTACHES TO THE
UVRA-UVRB COMPLEX, DISPLACING UVRA, AND THE DAMAGED DNA STRAND IS
NICKED ON BOTH SIDES OF THE DAMAGED SITE (BY SIMILARITY).
-!- SUBUNIT: CONSISTS OF THERE SUBUNITS; UVRA, UVRB AND UVRC.
-!- SUBCELLULAR LOCATION: CYtoplasmic (By similarity).
                                                                                                                                                                   Gaffney T.D., Lam S.T., Ligon J., Gates K., Frazelle A., Maio J.,
Hill S., Goodwin S., Torkewitz N., Allshouse A.M., Kempf H.J.,
                                                                                                                                                                                                                                                                                                                                                                            control in Pseudomonas fluorescens mediating antibiotic
                                                   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                          Laville J., Voisard C.P., Keel C., Maurhofer M., Difago G.,
                                                                                                                                                                                                                   "Global regulation of expression of antifungal factors by Pseudomonas fluorescens biological control strain."; Mol. Plant Microbe Interact. 7:455-463(1994).
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-> A (IN REF. 2).
179D412EC0B4398C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T -> A (IN REF. 2).
S -> N (IN REF. 2).
L -> Q (IN REF. 2).
G -> A (IN REF. 2).
E -> D (IN REF. 2).
E -> D (IN REF. 2).
E -> D (IN REF. 2).
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                                                                                                                                  STRAIN=BL915;
MEDLINE=94355677; Pubmed=8075420;
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Interpro; IPR000305; UVrC_1.
Pfam; PF01541; Exci_endo_N; 1.
Pfam; PF00633; HHH; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003583; HHH_1.
                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-232 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001943; UVR.
 Excinuclease ABC subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M80913; AAA25822.1
InterPro; IPR000445; HHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00465; GIYC; 1.
SMART; SM00278; HhH1; 2.
                                 Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                    SEQUENCE FROM N.A.
                                                                                  NCBI_TaxID=294;
                                                                    Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-JAL / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
MEDLINE=96337999; PubMed=8688087;
MEDLINE=96337999; PubMed=8688087;
Built C. J., Whithe O., Olsen G. J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FizzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
2-oxoglutarate synthase subunit KORB (EC 1.2.7.3) (2-ketoglutarate oxidoreductase beta chain) (KOR) (2-oxoglutarate-ferredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: 2-OXOBUTANOATE + COA + OXIDIZED FERREDOXIN PROPANOYL-COA + CO(2) + REDUCED FERREDOXIN.
-!- SUBUNIT: HETEROTETRAMER OF THE KORA, KORB, KORC AND KORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.3%; Score 45.5; DB 1; Length 270; 52.2%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tidk; Mideso; TPP_enzyme.
InterPro; IPPR000399; TPP_enzyme.
Pfam; PP02775; TPP_enzymes_C; 1.
Oxidoreductase; Complete proteome.
GROHENCE 270 AA; 29894 MW; 4F7331CF37216554 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
                                                                                                                                                 270 AA
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                          1 CGETYYSRVTHPHLPKDIVRSIAKC 25
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                                                                                                                                                                                                                                                                                                   oxidoreductase beta subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                           Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
                                                                                                                                               STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                    KORB OR MJ0537
                                                                                                                                                                                                                                                                                                                                                                                       Methanococcus
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                                                                                                                                                 KORB_METJA
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Indels

13:

Mismatches Score 46; Pred. No.

5

Conservative

Query Match Best Local Similarity Matches 10; Conserv

32.6%;

DB 1; Length 607;

097ip8 clostridium Q97x27 streptomyce Q927w8 drosophila Q9bLG9 trichinella Q9bLG9 trichinella Q9bLG9 trichinella Q9bLG9 trichinella Q9bLG9 arabidopsis Q40404 nicotiana p Q9FG2 nicotiana p Q9FG2 nicotiana p Q9FG2 nicotiana p Q9FG2 arabidopsis Q9InQ2 arabidopsis Q9InQ2 arabidopsis Q9InQ2 arabidopsis Q9InG2 arabidopsis Q9InG2 rattus norv Q9GG3 pyrococcus Q9GG3 rattus norv Q9GG3 rattus norv Q9GG3 rattus norv Q9GG1 lollum rigil Q94fF0 lollum rigil Q9AFG lollum rigil Q9AFG lollum rigil Q9AFG lollum rigil Q9GCNVC oryza sativ Q9GC29 erwina see

Total number of

Database

Searched:

Perfect score:

Run on:

Scoring table: Sequence:

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 283:2012-2018(1998). EMBL; 29287; CABO7326.1; -. InterPro: IPR004119; DUF227. Pfam; PF02958; DUF227; 1. SEQUENCE 394 AA; 44297 MW; D4424A972AE24451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54; DB 5; Length 394;
Pred. No. 4;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MCMurray A.A.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                 394 AA
                                                                                                                                                                                                                             ALIGNMENTS
             09977WB
09B1C9
09B1C9
040404
0404064
09FWGA
09HC4
0912D6
0912D6
0912D6
091270
093221
095221
094FS0
094FS0
094FS0
094FS0
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, C
01-JAN-1998 (TrEMBLrel. 05, L
01-DEC-2001 (TrEMBLrel. 19, L
C29F7.1 PROTEIN.
C29F7.1.
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60.0%;
110
110
110
110
                                                                                                          Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                 PRELIMINARY;
11 HPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 HPNLPKNVVIKIASC
Query Match
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                                                                                                                                                                                                                                                  RESULT
017620
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0084fr7 zea mays (m
008367 zea mays (m
048795 triticum ae
041743 zea mays (m
0901 pyrococus
0901 pyrococus
09120 arabidopsis
09127 mus musculu
09127 mus musculu
090544 qingiymosto
04165 zea mays (m
07504 homo sapien
04328 zea mays (m
07505 zea mays (m
                                                        (without alignments)
64.724 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                       O17620 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                 ; Search time 66.82 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                          Description
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                             hits satisfying chosen parameters:
                                                                                                                               562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                          1 CGETYYSRVTHPHLPKDIVRSIAKC
                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                  OM protein - protein search, using sw model
                                                 August 26, 2002, 10:16:17
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094FR6
094FR6
008367
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                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                   sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                 sp_unclassified:*
                                                                                                                                                                                                                                                                   sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                        sp_rvirus:*
sp_bacteriap:*
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sp_bacteria:*
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Maximum DB seq length: 200000000
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Match Length DB
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Score

Result No.

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Gaps

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RESULT Q94FR6

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                    Plant Mol. Biol. 24:35-49(1994).
-i- FUNCTION: THIS PROTEIN CARRIES THREE CATALYTIC FUNCTIONS: BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                      -:- CATALYTIC ACTIVITY: ATP + ACETYL-COA + HCO(3)(-) = ADP + ORTHOPHOSPHATE + MALONYL-COA.
-:- COFACTOR: BIOTIN.
-:- ENZYME REGULATION: BY PHOSPHORYLATION.
-:- PATHWAY: FIRST STEP (RATE LIMITING) IN LONG-CHAIN FATTY ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-B73; TISSUE-LEAF;
MEDLINE-94154242; PubMed-7906562;
Ashton A.R., Jenkins C.L., Whitfeld P.R.;
"Molecular cloning of two different cDNAs for maize acetyl CoA carboxylase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SQUENCE FROM N.A.
STRAIN-CV. HARD RED WINTER TAM 107;
MEDLINE-98054381; PubMed-9391173;
GORNICKI P., Faris J., Podkowinski J., Gill B., Haselkofn R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 1625;
18;
                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DC-2001 (TrEMBLrel. 19, Last annotation update)
ACETYL-COA CARBOXYLASE (EC 6.4.1.2) (ACC)
[CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14)] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                    PRT; 1625 AA.
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Pred. No. 1
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55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459 ETYISRLYQPHLVKDSIQ 476
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                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                           CARBOXYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                            Zea mays (Maize)
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                  008367
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                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zagnitko O., Jelenska J., Tevzadze G., Haselkorn R., Gornicki P.; "An isoleucine/leucine residue in the carboxyltransferase domain cactyl-CoA carboxylase is critical for interaction with aryloxyphenoxypropionate and cyclohexanedione inhibitors."; Proc. Natl. Acad. Sci. U.S.A. 98:6617-6622(2001).
                                                                                                                                                                                                                                                               Zagnitko O., Jelenska J., Tevzadze G., Haselkorn R., Gornicki P., "An isoleucine/leucine residue in the carboxyltransferase domain acetyl-CoA carboxylase is critical for interaction with aryloxyphenoxypropionate and cyclohexanedione inhibitors."; Proc. Natl. Acad. Sci. U.S.A. 98:6617-6622(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.3%; Score 54; DB 10; Length 1078; 55.6%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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1079 AA; 120717 MW; DAD7508EF9BE9AE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           120645 MW; 0ACFC8BE8D794CD1 CRC64;
                                                                                                                                                                                                                     SEQUENCE ...
STRAIN-CV. DK592;
MEDLINE-21287275; PubWed-11381131;
MEDLINE-21287275; PubWed-11381131;
Anionska J., Tevzadze G., Haselkorn R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  094FR7;
01-DEC-2001 (TEMBLrel. 19, Created)
01-DEC-2001 (TEMBLrel. 19, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
ACETYL-COA CARBOXYLASE (FRAGMENT).
                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.
 1078 AA.
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                                      Created)
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MEDLINE-21287275; Pubmed-11381131;
                                01-DEC-2001 (TrEMBLrel. 19, Created 01-DEC-2001 (TrEMBLrel. 19, Last so 01-DEC-2001 (TrEMBLrel. 19, Last and ACETYL-COA CARBOXYLASE (FRAGMENT).
                                                                                                                                                            Panicoldeae; Andropogoneae; Zea.
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55.6%;
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   PRELIMINARY;
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1078 AA;
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Best Local Similarity
Matches 10; Conserva
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Matches 10; Conserv
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STRAIN=CV. COLUMBIA;
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Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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InterPro; IPR003653; SUMO_protease.
Pfam: PF02902; U1p1_C: 1...
SEQUENCE 1756 AA: 197368 MW; 68FC3B5FCC282775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR000051; SAM_bind.
Hypothetical protein; Complete proteome.
SEQUENCE 195 AA: 21778 MW; 471178A62097C02C CRC64;
                                                              Last sequence update)
Last annotation update)
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 21.8 KDA PROTEIN.
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Pred. No. 5.5;
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                                      Created)
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Best Local Similarity 47.8%;
Matches 11; Conservative
                                      08,
08,
19,
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                                   01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
AT2G14770 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
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                                                                                                                                             AT2G14770.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
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"Plastid-localized acetyl-CoA carboxylase of bread wheat is encoded to single gene on each of the three ancestral chromosome sets.";
Proc. Natl. Acad. Sci. U.S.A. 94:14179-14184(1997).
EMBL, AF029895; AAC39330.1; -.
EMBL, AF029896; AAC39330.1; -.
HSSP; P24182; 1DV1.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000091; CRSase.
InterPro; IPR000901; CRSase.
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                                                                                                                                                                                                                                                                                          Pfam; PF01039; Carboxyl_trans; 1.
Pfam; PF00289; CPSase_L.chain; 2.
Pfam; PF00786; CPSase_L.D2; 1.
PROSITE; PS00867; CPSASE_2; UNKNOWN 1.
SEQUENCE 2311 AA; 254970 MW; IBBC5CDD0F9F984B CRC64;
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PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
SEQUENCE 2325 AA; 257150 MW; ECEOAEF3FE26FE0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A188; TISSUE-LEAF;
MEDLINE-95357420; PubMed=7630949;
Egli M.A., Lutz S.M., Somers D.A., Gengenbach B.G.;
"A maize acetyl-coenzyme A carboxylase cDNA sequence.";
Plant Physiol. 108:1299*1300(1995).
EMBL; U19183; AA860214.1; -.
HSSP; P24182; 1DV1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ACETYL-COENZYME A CARBOXYLASE.
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27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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55.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.3%; Score 54; 55.6%; Pred. No.
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InterPro; IPR000022; Carboxyl_trans.
InterPro; IPR000901; CPSase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; L. Panicoideae; Andropogoneae; Zea NCBI_TaxID-4577;
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1158 ETYISRLYQPHLVKDSIQ 1175
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 10; Conserv
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Wong K., Ren X.-R., Huang Y.-Z., Xie Y., Liu G., Saito H., Tang H., Wen L., Brady-Kalnay S.M., Mei L., Wu J.Y., Xiong W.-C., Rao Y.; Signal Transduction in Neuronal Migration: Roles of GTPase Activating Proteins and the Small GTPase Gdc42 in the Slit-Robo Pathway."; cell 107:209-221(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C., Flajnik M.F.;
"A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";
Nature 374:168-173(1995).
BMBL: U18701; AR48195:1;
HSSP; P01709; 2MCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ginglymostoma cirratum (Nurse shark).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes; Ginglymostomatidae; Ginglymostomatidae; Ginglymostomat
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                             Length 539
                                                                                                            Indels
              Hypothetical protein.
SEQUENCE 539 AA; 59412 MW; FCA23BA0BC9ECE2E CRC64;
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                                                                                                                                                                                                                                                                   Q91267;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAP2 (FRAGMENT)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NOVEL ANTIGEN RECEPTOR PRECURSOR.
                                                                                                          ٠<u>.</u>
                                                                             10;
                                                                           score 50; DB 1; Pred. No. 23; 7; Mismatches
                                                                                                                                                                                                                                                     405 AA.
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MEDLINE=21526632; PubMed=11672528;
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MEDLINE=95183140; PubMed=7877689;
                                                                                                                                         1 CGETYYSRVTHPHLPKDIVRSIAK 24
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| 37 YFRGLEHPLFPKDIFHDLIAC 157
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38.1%;
                                                                         35.5%;
illarity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
SMART; SM00288; VHS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 AA;
                                                                             Ouery Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                    Q91267
                                                                                                                                                                                                                        RESULT 11
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                                                                                                                                                                                                                                                                                                                                                Drummelsmith J., Whitfield C.; "Gene products required for surface expression of the capsular form of the group 1 K antigen in Escherichia coli (O9a:K30)."; Mol. Microbiol. 31:1321-1332(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.2%; Score 51; DB 2; Length 416; 52.4%; Pred. No. 12; 7; Indels tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DrumenIsmith J., Whitfield C.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104912; AAD21570.2; -.
SEQUENCE 416 AA; 47432 MW; 1C903B56E52EFF20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL162351; CAB82746.1; -.
IfterPro; IFR002014; HRS.
Pfam; PF00790; VHS; 1.
                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
K30 CAPSULE BIOSYNTHESIS CLUSTER, PARTIAL SEQUENCE.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 59.4 KDA PROTEIN.
                                                                                                                          416 AA.
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                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                               MEDLINE-99217011; PubMed-10200954;
                               119 GEKFHSIITNPPVHAGKDILREI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 TYEKGVTHIFVDKDKIRSISK 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TYYSRVTHPHLPKDIVRSIAK 24
              2 GETYYSRVTHP--HLPKDIVRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD003686; HRS; 1
                                                                                                                          PRELIMINARY;
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nes 11; Conserv
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NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
                                                                                                                                         Q9X4C5;
01-NOV-1999
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Q9L2X0;
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Matches
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Gaps

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Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Addropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                         Sexi N., Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D., Nomira N., Ohira O.;
Nomira N., Ohira O.;
Ishikawa F., Ishikawa F., Miyajima N., Nakajima D.,
Ohira O.;
Ishikawa C.;
Ishikawa F., Miyajima N., Nakajima D.,
Ishikawa C.;
Ishikawa C.;
Ishikawa C.;
Ishikawa Jafe 349(1997).
Ishikawa Ses. 4:345-349(1997).
Ishikawa Ses. 4:345-349(1997).
InterPro: Ishikawa C., Nakaya J.;
InterPro: Ishikawa C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-B73; TISSUE-LEAF;
MEDLINE-9415-42; PubMeds
Ashton A.R., Jenkins C.L., Whitfeld P.R.;
"Molecular cloning of two different cDNAs for maize acetyl CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49; DB 10; Length 1685; Pred. No. 1.1e+02; 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 4; Length 1095;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50002; SH3; 1.
NON_TER 1 1 123752 MW; 27A8AD852B62B1A0 CRC64; SEQUENCE 1095 AA; 123752 MW; 27A8AD852B62B1A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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EMBL: U58598; AAB01188.1; -.
Interpro: IPR000089; Biotin_lipoyl.
Interpro: IPR000022; Carboxyl_trans.
Pfam; PF00364; biotin_lipoyl, 1.
Pfam; PF01039; Carboxyl_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187594 MW; 516BBB4B7CA7B116 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ACETYL COA CARBOXYLASE (EC 6.4.1.2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1685 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                            TISSUE=BRAIN;
MEDLINE=98116662; PubMed=9455484;
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Plant Mol. Biol. 24:35-49(1994).
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592 YFRGLEHPLFPKDIFHDLMAC 612
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38.1%;
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52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00055; FCH; 1.
SMART; SM00324; RhoGAP; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
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STRAIN-B73; TISSUE-LEAF;
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Matches 9, Conserv
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SEQUENCE FROM N.A.
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SEQUENCE
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Q43248
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Bukaryocts; Uridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID-9606;
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Pred. No. 69;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1078 AA; 120560 MW; B76F56B4CC608E4E CRC64;
                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
NOVEL ANTIGEN RECEPTOR.
2 2FF9D2071CDA6DFD CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49;
Pred. No. 4
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 6
SMART; SM00407; Igc1, 4
SMART; SM00410; Ig_like; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
ACETYL-COA CARBOXYLASE (FRAGMENT).
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MEDLINE-21287275; PubMed=11381131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        642 TYSCLVGHPSLNRDLIRSTNK 662
                                                                                                                                                                                                                                                                                                                                                                                 684 NW;
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52.98;
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Best Local Similarity 47.6
Matches 10; Conservative
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Best Local Similarity 52.9
Matches 9; Conservative
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SEQUENCE
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Copyright (c) 1993 - 2000 Compugen Ltd.

    protein search, using sw model

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747574 segs, 111073796 residues 141 1 CGETYYSRVTHPHLPKDIVRSIAKC 25 Gapop 10.0 , Gapext 0.5 us-09-701-623C-6 BLOSUM62 Perfect score: Scoring table: Sequence: Searched: Title:

747574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_032802:* Database :

/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
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/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:* 14: 116: 117: 118: 119: 120: 120:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Optimised IqE-CH3	IqE immunogenic pe	IqE immunodenic pe	IqE immunogenic pe	IqE immunogenic pe	IqE immunogenic pe	IdE immunogenic pe	Partial canine imm	Dog immunoglobulin	Immunogenic peptid	Canine IgE heavy c
ID	AAY79999	AAY80019	AAY80083	AAY80020	AAY80081	AAY80080	AAY80084	AAW24097	AAY79995	AAB06208	AAW23067
98	21	21	21	21	21	21	21	18	21	21	18
Query Match Length DB ID	25	45	45	46	57	62	63	124	312	341	417
Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	83.7	83.7	83.7	83.7
Score	141	141	141	141	141	141	141	118	118	118	118
Result No.	П	2	m	4	S	9	7	æ	6	10	11

Canine IgE. Canis Optimised IgE-CH3 Modified human IgE Peptide sequence o IgE immunogenic pe Modified MVF Th ep	MVF Th MVF Th sequence	Modified HBV surfa Peptide sequence o IgE immunogenic pe	Modified MVF Th ep Modified MVF Th ep Peptide sequence o	Lmmu Lmmu	immunogenic -CH3 domain a immunogenic	Inv epitope/modifi Peptide sequence o Optimised IgE-CH3	Optimised 19E-CH3 19E immunogenic pe Canine immunoglobi	Immunogenic peptid Antibody 15A.2 bin Antibody 15A.2 can	IgE - m E Fceps psilon
AAR97753 AAY79998 AAY91212 AAY68602 AAY80014	AAY91216 AAY91217 AAY68604	AAY91218 AAY68605 AAY80011	AAY91213 AAY91214 AAY68603	AAY80016 AAY80010 AAY80013	AAY80015 AAY80008 AAY80012	AAY91219 AAY68606 AAY80000	AAY80077 AAY80078 AAW24102	AAY50893 AAY50894	AAR33324 AAY42620 AAR33304
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83.7 76.6 76.6 76.6 76.6	9999				999	76.6 76.6 74.5		64.5 61.0 61.0	
118 108 108 108 108	108 108 108	108 108 108	108 108 108	108	108 108 108	108 108	105 101 95	91 86 86	8 8 8 5 8
12 13 14 15 17	18 19 20	22 23 24 34	25 26 27	28 30	33 33 33	34 36 36	37 38 39	4 4 4 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	43 44 45

ALIGNMENTS

Optimised IgE-CH3 domain antigen peptide for dog IgE. AAY79999 standard; Peptide; 25 AA. 15-MAY-2000 (first entry) AAY79999; RESULT AAY79999

Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anti-arathmatic; asthma; anaphylaxis; dermatitis.

99WO-US13959 98US-0100287 21-JUN-1999; 20-JUN-1998; W09967293-A1 29-DEC-1999. Canis sp. Synthetic.

(UNBI-) UNITED BIOMEDICAL INC. Wang CY, Walfield AM; WPI; 2000-160578/14. New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy $\,$

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                                                    present invention describes immunoglobulin E (IgE)-CH3
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Pred. No. 1.2e-14;
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                Claim 1; Page 99; 155pp; English.
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and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. ARY79994 to AAR90084 represent amino acid sequences used in the exemplification of the present invention.
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Pred. No. 2.3e-14;
0; Mismatches 0;
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antigenic peptides (1). (1) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (1) induces polyclonal antibodies specific for a target effector site on the peptiden heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (1) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (1) that include a promiscuous Thelper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. NAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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(functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity, and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigenic peptide from the CH3 domain of immunoglobulin E, fusions immunization against allergy -
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2.3e-14;
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Pred. No. 2.3e
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Matches 25; Conser
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                                                                                                                                                                                                                                                                                                                                           immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
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100.0%; Pred. No. 3.1e-14;
iive 0; Mismatches 0;
 Score 141; DB 21;
Pred. No. 2.4e-14;
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100.0%;
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Best Local Similarity
Matches 25; Conserv
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antigence peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of 1gE, and so preventing triggering and activation of mast cells and basophils and so preventing triggering and activation of mast cells and basophils and downregulation of 1gE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against 1gE-mediated allergies, e.g. food allergies, action in anaphylaxis, or float-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies, AAY79994 to AAX80084 represent amino
                                                                                                                                                                                                  Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-ashthatic; asthma; anaphylactic; anti-ashthatic; asthma; anaphylaxis; dermatitis.
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                                                                                                                                                   [gE immunogenic peptide conjugate SEQ ID NO:91.
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100.0%; Pred. No. 3.4e-14;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                              IgE immunogenic peptide conjugate SEQ ID NO:87.
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1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                         33 cgetyysrvthphlpkdivrsiakc
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Length 63; Indels

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                                                                                                                                                                                           This is a partial canine immunoglobulin E (IgE) protein. Peptide fragments (AAW24098-106) containing at least five continuous amino acids of this sequence are used for the preparation of anti-canine IgE antibody. The anti-canine IgE antibody can be used for the diagnosis of canine allergies.
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        Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.
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                                                                                                                                                    Canine immunoglobulin E peptide fragment and related DNA - useful for the preparation of anti-canine immunoglobulin {\tt E} antibody
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95.7%; Pred. No. 2.5e-10;
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Best Local Similarity
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N-PSDB; AAT85646.
                                                                                                                                                                                                                                                124 AA;
                        Canis familiaris.
                                         JP09169795-A
                                                                          22-DEC-1995;
                                                                                           22-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09967293-A1
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                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-2000
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                                                          30-JUN-1997
                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                     AAY 79995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis sp
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antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the dog. It was shown to cause a stronger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy; asthma; eczema; immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                        present invention describes immunoglobulin E (IgE)-CH3 domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.7%; Score 118; DB 21;
95.7%; Pred. No. 7.4e-10;
tive 0; Mismatches 1;
Example 1; Page 66-68; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB06208 standard; protein; 341 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 getyycrvthphlpkdivrsiak 209
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Chimeric - Canis sp.
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99US-0401636.
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Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Disclosure; Page 35-39; 59pp; English.
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                                                                                                                                                                                                                            AAR97753;
                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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polycional anti-self IgE response than peptides consisting of the same
        regions from one mammal. Immunogenic peptides, particularly those constating of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated canine IgE heavy chain constant region DNA - useful to develop products for treatment of canine allergies and for immunomodulation in dogs
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                                                                          Length 341;
                                                                                                                                                                                                                                  IgE; immunoglobulin; antibody; heavy chain constant region; allergy; hypersensitivity; therapy; dog; antisense; immunomodulation.
                                                                                                                                                                                                                   Canine IgE heavy chain constant region (exon 1-4 product).
                                                                                           Indels
                                                                          Score 118; DB 21;
Pred. No. 8.2e-10;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                   'note= "encoded by ACC"
                                                                                                                                                                                                                                                                                                                   'note- "encoded by TAC"
                                                                                                                                                                                                                                                                                                                                    'note- "encoded by GCC"
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                                                                                                                                                                                                                                                                                                                                                                                    by NNG"
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                                                                                                                   AAW23067 standard; Protein; 417
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                                                                                                           GETYYSRVTHPHLPKDIVRSIAK
                                                                          83.7%;
95.7%;
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                                                                                                                                                                                                    (first entry)
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harris RA, Mermer B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IDEX-) IDEXX LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-425031/39.
N-PSDB; AAT79278.
                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 176
                                                                                                                                                                                                                                                                                                                                                           Misc-difference 174
                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 175
                                                                                 Similarity
                                                                                                                                                                                                                                                                                            Misc-difference 55
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                                                                                                                                                                                                                                                                                                                                           Misc-difference 83
                                                  341 AA;
                                                                                                                                                                                                                                                                   Canis familiaris.
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                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                           22;
                                                  Sequence
                                                                                                                                                                                   AAW23067;
                                                                          Query Match
Best Local 8
                                                                                                                          206
                                                                                           Matches
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This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE heavy chain constant region (epsilon) genomic DNA. Another polypeptide, comprising the exon 5 and 6 product, is given in AAW23068. Recombinant peptides encoded by exons 1-6 can be produced in eukaryotic or prokaryotic cells. Such peptides, and antibodies raised against them, are used in methods to treat the manifestation of allergy in dogs, e.g. to treatment Type I immediate hypersensitivity, and for immunomodulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The canine IgE amino acid sequence (AAR97753) was deduced from an isolated gene (AAT29824) obtd. from a canine liver DNA library. The cloning of the IgE gene allows prodn. of large quantities of recombinant IgE using bacterial, yeast, mammalian, insect or viral systems. The IgE can be used in drug development (e.g. small molecule screening, assay development and anti-IgE antibody generation). Fragments of IgE can be used in vaccines or to prevent IgE-mediated hypersensitivity. The new sequence information permits targeted modulation of IgE-mediated immune
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                                                                                                                                                                                                                                                                                                                                                                              Length 417;
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                                                                                                                                                                                                                                                                                                                                                                              Score 118; DB 18;
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); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 getyycrvthphlpkdivrsiak 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR97753 standard; Protein; 426
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                                                                                                                                                                                                                                                                                                                                                                              83.7%;
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94US-0336583,
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N-PSDB; AAT29824.
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                       417 AA;
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09-NOV-1994;
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DB 17; Length 426;

83.7%; Score 118;

Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigon; HBV; immunogenic; B-cell epitope; lutelnising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic; Plasmodium falciparum; circumsporcoxite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.

Homo sapiens

Synthetic.

W09966957-A2

29-DEC-1999.

Modified human IgE CH3 domain, SEQ ID NO:92.

(first entry)

22-MAY-2000

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AAY91212;

AAY91212 standard; peptide; 25 AA.

AAY91212 RESULT

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antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and soo preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous Thelper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino conformation.
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                                                                                                                                                                                                                                                                                                                                     Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobulinulatory: carrier protein; helper T cell epitope; antibody; allergy: allergy: disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes immunoglobulin E (IgE)-CH3 domain
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0
                                      Indels
                                                                                                                                                                                                                                                                                                   Optimised IgE-CH3 domain antigen peptide for human IgE.
 Pred. No. 1.1e-09;
                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 21; 155pp; English.
                                                                                          289 getyycrvthphlpkdivrsiak 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunization against allergy
                                                                      2 GETYYSRVTHPHLPKDIVRSIAK 24
                                                                                                                                                                                              AAY79998 standard; Peptide; 25
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f.
Best Local Similarity 95.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US13959
                                                                                                                                                                                                                                                                  15-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Walfield AM;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                                                               AAY79998;
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                                                                                                                                                            RESULT
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The invention relates to novel promiscuous T helper cell epitopes (Th),
and immunogenic peptides comprising the Th epitopes of the invention
along with B cell epitopes. The Th epitopes and peptide immunogens
containing them, are used to induce a T helper cell response,
specifically against Plasmodium falciparum, cholesteryl ester transport
containing them, are used to induce a T helper cell response,
specifically against Plasmodium falciparum, cholesteryl ester transport
containing them, are used for prevention and/or treatment of
immunocens may be used for prevention and/or treatment of
infections (HINY, foot-and-mouth disease or malarals); for cancer
containing hormone (LHRH) for contraception, treatment of hormone
containing hormone (LHRH) for contraception, treatment of hormone
contraction); for promoting the growth of animals; or for
immunocastration); for promoting the growth of animals; or for
treating allergies or arteriosclerosis. Incorporation of a promiscuous
contraction in genetically diverse subjects) into an immunogen
contraction in production of antibodies against a target
consect resulting in production of antibodies against a target
consect resulting in production of antibodies against a target
consect resulting in production of antibodies against a target
consect resulting in production of antibodies against a target
consect resulting in production of antibodies against a target
constitute an replace carrier proteins and seduences Aay91122-191144.

Aay9125 and AAy91245-19144 represents a promiscuous Th epitope
from the measles virus F (MVF) protein and sequences
comprising an LHRH sequence AAy91143 represents a promiscuous Th epitope
comprising an LHRH sequence Johned to a promiscuous Th epitope.
AAY91156-Y91164 AAY91227 and AAY91241-404 are antigenic
comprising an LHRH target antigenic peptide used in these LHRH target antigenic peptides comprising somatostatin, and a Th epitope. Sequence peptides comprising somatostatin, and a Th epitope.
Comprising the LHRH requer antigenic and the promiscu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Page 40; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0100412.
                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US13975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-160564/14.
                                                                                                                                                                                                                                                                                                                                                                                                          21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-1998;
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Gaps

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Indels

4,

3; Mismatches

1 CGETYYSRVTHPHLPKDIVRSIAKC 25

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Conservative

Query Match Best Local Similarity Matches 18; Conserv

76.6%; Score 108; DB 21; Length 25; 72.0%; Pred. No. 1.3e-09;

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chilerope/CD4 CDR2 antigenia peptides which may be used to prevent HIV
chilerope/CD4 CDR2 antigenia peptides which may be used to prevent HIV
cells. AAY90212 is a modified version of a human IgE
(immunoglobulin B) CH3 domain, and AAY90213-Y90219 are Thepitope/TgE CH3
antigenic peptides which may be used in the treatment of alleropes/TgE CH3
AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
vPl capsid protein and AAY91221-Y91222 comprise this peptide and a Th
ceptiope and may be used in a malaria vaccine. AAY91228-Y91231 represent
CETP peptide and aTh epitope which may be used to prevent or treat
cETP peptide and aTh epitope which may be used to prevent or treat
arterioscierosis and cardiovascular disease. AAY9124-Y91251 and AAY91257
arterioscierosis and cardiovascular disease. AAY9124-Y91251 and AAY91257
arterioscierosis and cardiovascular disease. AAY9124-Y91251 and AAY91257
arterioscierosis and cardiovascular disease. AAY9124-Y91251 and AAY91256-Y91273 are antigenic peptides comprising WNH Th and HIV-1 B-cell
comprise which may be used as a component in an anti-HIV-1 vaccine.
AAY91198 and AAY91199 are respectively an immunostimulatory invasin
c protein epitope from Yersinia species, and hinge spacer peptide, both of
which may optionally be used in the antigenic peptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helper T cell epitope; peptide immunogen; LHRH;
luteinising hormone-releasing hormone; spermatogenesis; ovulation;
oestrus; sexual development; sex hormone; promiscuous T helper epitope;
vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
breast cancer; endometriosis; boar taint; meat quality; immunocastration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes peptide immunogens comprising a synthetic helper T cell (Th) epitope and a target antigen, luteinising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.6%; Score 108; DB 21; Length 25; 72.0%; Pred. No. 1.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 92; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY68602 standard; peptide; 25 AA.
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Matches 18; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                        25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                     Invention.
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              induction of a specific immune response to LiRH which is involved in regulation of spermatogenesis, ovulation, oestrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent boar taint (and improve meat quality) and for immunocastration. The present sequence appears in the specification.
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hormone-releasing hormone (LHRH). The peptide immunogens cause
                                                                                                                                                                                                                                                                                                                       Length 25;
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Pred. No. 1.3e-09;
3; Mismatches 4;
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ne: 227 sec
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72.08;
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APPII APPII APPII APPII APPII APPII APPII APPII

Sequence 3 Sequence 3 Sequence 2 Sequence 2

Sequence 3 Sequence 3 Sequence 3

Sequence:

Run on:

Searched:

Sequence 9, Ag Sequence 6, Ag Sequence 6, Al Sequence 6, Al Sequence 17, Sequence 11, Sequence 17, Sequence 17, Sequence 11, Al

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Score 118; DB 1; Length 426;
Pred. No. 3.1e-11;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08336583
Patent No. 5629415
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN INUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: LOUDS-USOU

COMPUTER: FLORPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC COMPA:

COMPUTER: IBM PC COMPA:

COMPUTER: IBM PC COMPA:

COMPUTER: DATE: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/336,583

FLING DATE: 09-NOV-1994

ATTON NEY/AGENT INFORMATION:

NAME: CARTY. CHRISTINE E.

REGISTRATION NUMBER: 36,099

REGISTRATION NUMBER: 36,099

REJERBENCE/COCKET UNMBER: 36,099

RELECOMMUNICATION INFORMATION:

TELECOMMUNICATION SEQ ID NO: 2:

COMPUTER: CARTY CHRISTINE

TELECOMMUNICATION SEQ ID NO: 2:
US-08-934-386-9
US-08-617-089-6
US-08-6930-285-6
US-08-695-421-6
US-08-695-421-17
US-09-130-330-11
US-09-130-330-1
US-08-77-010-3
US-08-77-010-3
US-08-790-519-3
US-08-790-519-3
US-08-790-519-3
US-08-119-31
US-08-46-981-6
US-08-46-981-6
US-08-488-161-31
US-08-488-161-31
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Best Local Similarity 95.7
Matches 22; Conservative
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  , MOLECULE TYPE: protein US-08-336-583-2
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STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-303-323-95
US-09-100-414B-98
US-09-303-323-98
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US-09-303-323-100
US-09-303-323-101
US-09-303-323-101
US-09-100-414B-95
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US-08-232-539D-19
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Maximum Match 100%
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 95, Application US/09303323;
Fatent No. 6228947;
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: STREET: 345 Park Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
                                                                                                                              1151-4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGETYYSRVTHPHLPKDIVRSIAKC 25
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ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REGISTRATION NUMBER: 1151-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 25 amino acids
TYPE: amino acids
US-09-100-4148-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC Windows
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REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-09-303-323-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-303-323-95
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                                                      GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
CORRESPONDENCE ADDRESS: A
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
CITY: RAHMAR.
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 07056-0907
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NAMBER: PCT/US95/13795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 95, Application US/09100414B
| Patent NO. 6025468
| GENERAL INFORMATION:
| TITLE OF INVENTION: IMMUNOGENS
| TITLE OF INVENTION: IMMUNOGENS
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: MOOFGAN & Finnegan, L.L.P.
| STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: WORD 97
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GETYYSRVTHPHLPKDIVRSIAK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein PCT-US95-13795-2
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Best Local Similarity
Matches 22; Conserva
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-09-100-414B-95
                     RESULT 2
PCT-US95-13795-2
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STATE:
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Gaps
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Sequence 100, Application US/09100414B
Fatent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: INMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                               SOUTHWARE: WOLD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/09/100,414B
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC COMPALIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: WOR'D 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100.
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
                                     E: Floppy disk
IBM PC compatible
SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: "TATORIES ATTORIES MARIA H. LÎN REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 42 amino acids TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
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                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                           amino acid
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                               US-09-100-414B-99
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Matches
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                      Gaps
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Best Local Similarity 72.0%; Pred. No. 4.6e-11;
Matches 18; Conservative 3; Mismatches 4; Indels
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Sequence 99, Application US/09100414B

Sequence 99, Application US/09100414B

Patent No. 6023468

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: IMMUNOGENS

NUMBER OF SEQUENCES: 106

CORRESPONDENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.

STREET: 345 PATK AVenue

CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                     Sequence 98, Application US/09100414B
Fatent No. 6025468
GENERAL INFORMATION:
TITLE OF INVENTION: INMUNOGENS
TITLE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                        1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 CGETYQSRVTHPHLPRALMRSTTKC 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.0%
Matches 18; Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-09-100-414B-98
                                                                                                                                                                                                                                                                                                                                                                                      COUNTR: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                      US-09-100-414B-98
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NUMBER OF SEQUENCES:
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                                                                                                                         COUNTRY: USA
ZIP: 10154-0054
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10154-0054
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US-09-303-323-100
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COUNTRY:
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                                                            Score 108; DB 3; Length 42; Pred. No. 8.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.6%; Score 108; DB 4; Length 42; Best Local Similarity 72.0%; Pred. No. 8.5e-11; Matches 18; Conservative 3; Mismatches 4; Indels
                                                                                                       4; Indels
                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                 Sequence 98, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
GAPPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: INMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09,100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. LIN
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECHONE: 212-758-4800
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Sequence 99, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
                                                                                                                                          1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                    1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.68;
72.08;
                                                        Query Match
Best Local Similarity 72.0%
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-09-303-323-98
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US-09-100-414B-100
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US-09-303-323-98
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 108; DB 4;
Pred. No. 8.5e-11;
3; Mismatches 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 100, Application US/09303323
Patent No. 6228987
GENERL INFORMATION:
TITLE OF INVENTION: INWAUNOGENS
TITLE OF INVENTION: INWAUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                 ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
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CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1151-4157
                                                                                                                                                                                                                                                                                                                                        FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTONNEY/ABOTT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-41:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGETYYSRVTHPHLPKDIVRSIAKC 25
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MEDIUM TYPE:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-09-303-323-99
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:

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76.6%; Score 108; DB 4; Length 45; 72.0%; Pred. No. 9.2e-11; tive 3; Mismatches 4; Indels
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Sequence 96, Application US/09100414B
Fatent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: INMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                Sequence 101, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNA JAGENT INFORMATION:
NAME: MATIA H. LIN
REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 CGETYQSRVTHPHLPRALMRSTTKC 45
                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 72.09
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-101
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Word 97
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                   ZIP: 10154-0054
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 3(CLASSIFICATION:
                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                    STATE:
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Pred. No. 9.2e-11;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                    Length 42;
                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                 Score 108; DB 4;
Pred. No. 8.5e-11;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 101, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: INMUNOGENS
TITLE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTGAN & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFRAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                          18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 CGETYQSRVTHPHLPRALMRSTTKC 45
                                                                                                                                                                                                                                                                                                                                     1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                  | INFORMATION FOR SEQ ID NO: | SEQUENCE CHARACTERISTICS: | LENGTH: 42 amino acids | TYPE: amino acid | TYPE: amino acid | TOPOLOGY: linear | MOLECULE TYPE: peptide | US-09-303-323-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 101: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.6%;
                                                                                                                                                                                                                                                               Query Match 76.6%;
Best Local Similarity 72.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.68
Best Local Similarity 72.03
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-09-100-4148-101
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76.6%; Score 108; DB 3; Length 46; 72.0%; Pred. No. 9.5e-11;
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Pred. No. 9.5e-11;
3; Mismatches 4;
                                          3; Mismatches
                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APTICATION NUMBER:
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MATIAH H. LID
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-758-4800
TELECHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: August 26, 2002, 10:05:18
Job time: 124 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
                                                                                                                                                                                     RESULT 15
US-09-303-323-96
Sequence 96, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
                                                                                                          22 CGETYQSRVTHPHLPRALMRSTTKC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 CGETYQSRVTHPHLPRALMRSTTKC 46
                                                                                    1 CGETYYSRVTHPHLPKDIVRSIAKC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: NY
COUNTRY: USA
ZTP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
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Best Local Similarity 72.04
Matches 18; Conservative
                   Best Local Similarity 72.08
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-09-303-323-96
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3Y: linear
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 97, Application US/09100414B
Patent No. 602546B
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
                          CURRENT APPLICATION DATA:
SOFTWARE: WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-UNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MALIA H. Lin
REGISTRATION NUMBER: 29,323
REFRENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
INFORMATION FOR SEC ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 aniloo acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97

CURRENT APPLICATION DATA:
APPLICATION DATA: 20-JUNE-1998

CLIASSIFICATION: 424
ATTONNEY, AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 29,323

REFERENCE/POCKET NUMBER: 1151-4157

TELECHONE: 212-751-6849

ITELEPHONE: 212-751-6849

INFORMATION DOCES IN NOT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 CGETYQSRVTHPHLPRALMRSTTKC 46
IBM PC compatible
SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.6%;
Best Local Similarity 72.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 amino acids
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
HOLECULE TYPE: peptide
US-09-100-414B-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                                                             amino acid
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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US-09-100-4148-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-100-414B-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: P
COUNTRY:
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Gaps

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Length 46; Indels

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(without alignments) 52.370 Million cell updates/sec
                                                                                                                                                                  August 26, 2002, 10:04:24; Search time 45.87 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                  Run on:
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145 1 CGEGYQSRVDHPHFPKPIVRSITKC 25 BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-701-623C-7 Perfect score: Scoring table: Sequence:

283138 Total number of hits satisfying chosen parameters: 283138 segs, 96089334 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries pirl:* pir2:* pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Query Match Length DB Score Result No.

1 1 1 1						
7	122	84.1	429	н	EHRT	Iq epsilon chain C
~	98		107	~	I68730	chain C3
9	86	9. 79	107	7	168726	IgE chain C3 regio
4	98	ζ.	388	Н	EHMS	epsilon ch
2	86	۲.	548	~	S38864	epsilon
9	82	œ.	423	-	EHMSS	epsilon
7	83	ζ.	426	N	I36948	epsilon-
œ	80	'n.	428	Н	ЕННО	Ig epsilon chain C
6		ъ.	245	7	155951	class II
10		'n	264	7	A60497	H-2 class II histo
11			264	~	S10989	ss II hist
12			345	Н	HLCHB4	MHC class I histoc
13		33.8	355	7	151309	hist
14		ω.	355	7	T28149	MHC class I histoc
15	49	ω.	355	~	T28152	ass
16	49	ش	430	7	AG0531	cell cycle protein
17	49	33.8	549	~	S04845	Ö
18	49	ω.	1208	0	T23222	pothetical pr
19	8	33.4	267	7	T33400	kinas
20	48.5	33.4	297	7	T33399	protein kinase C h
21	8	33.4	704	Н	S60117	protein kinase C (
22		33.1	93	~	154421	MHC RT1.B-beta2 -
23	48	33.1	110	~	S43147	g upsilon
24	48	33.1	152	N	S14236	Ig gamma-1 chain C
25	48	33.1	237	7	C60497	
56	48	33.1	566	~	A39260	MHC class II histo
27	48	33.1	266	N	B39260	MHC class II histo
28	48	33.1	324	-	GIMS	Ig gamma-1 chain C
29	48	33.1	393	÷	G1MSM	б

monoclonal antibod hypothetical prote	Ig gamma-2a chain hypothetical prote protein T6D22.14 [hypothetical prote hypothetical prote probable cardiolin	hypothetical prote desulfoferrodoxin BoLA-DQ beta-1 - b	MHC cell surface g 32K nonstructural multidrug resistan	Ig gamma 3 chain c Ig gamma 1 chain c
PC4436 T49726	PS0019 T26467 D86215	AG2525 E86267 E97307	D84566 E64392 A45544	145938 MNIH32 AB3610	147161 147158
777	000	000	1000	0 11 0	77
444	322 1413 2254	302	86 116 238	260 277 314	328
33.1	32.4 32.4 32.4	32.1 32.1	31.7 31.7 31.7	31.7 31.7 31.7	31.7 31.7
48	47 47 74	4 4 4 6 .5 6 .5 6 .5 6 .5 6 .5	4 4 4 0 9 9	4 4 4 6 6 6	46 46
30	33 34 34	35 36 37	388 409	41 42 43	44

ALIGNMENTS

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A; Molecule type: mRNA
A; Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction
A; Reference number: A90937; MUID:83182019
A; Molecule type: mRNA
A; Mole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;118-186/Domain: immunoglobulin homológy <IM2>
F;223-291/Domain: immunoglobulin homology <IM3>
F;327-398/Domain: immunoglobulin homology <IM4>
F;36,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Ig epsilon chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accession: A93442; A90937; A02143
R;Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6649, 1982
A;Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
A;Reference number: A93442; MUID:83064537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 84.1
Best Local Similarity 95.7
Matches 22; Conservative
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ö 2 GEGYQSRVDHPHFPKPIVRSITK 24 ð

284 GEGYQCRVDHPHFPKPIVRSITK 306 Db

RESULT

C.Species: Mus musculus (house mouse) C.bate: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000 C.Accession: 168730 R.Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K. Immunogenetics 27, 288-292, 1988 A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic aci A;Reference number: 154443; MUID:88152907 168730 IgE chain C3 region - mouse (fragment)

2002

26 11:09:32

Mon Aug

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Employed the chain C region (version 2) - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Jo-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
C; Accession: A02145
BRD J. 1. 1171-1123, 1982
BRD J. 1. 1171-1123, 1982
A; Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison A; Reference number: A90966; MuID: 84236092
A; Accession: A02145
A; Accession: A02145
A; Moccule type: DNA
A; Residues: 1-423 < ISH>
A; Note: the sequence was determined from the germline gene
C; Genetics:
A; Introns: 91/1; 199/1; 307/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin C region; immunoglobulin homology < IMM2>
F; 16-77/Domain: immunoglobulin homology < IMM2>
F; 16-77/Domain: immunoglobulin homology < IMM3>
F; 250-288 / Domain: immunoglobulin homology < IMM4>
F; 23-75/Domain: immunoglobulin homology < IMM4 </p>
F; 23-75/Domain: immunog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cybres. Objects. May State Mouse, Mou
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          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 548;
          Indels
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Pred. No. 1.8e-06;
0; Mismatches 4;
          4,
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llarity 77.3%; Pred. No. 0.00011;
Conservative 0; Mismatches 5;
          Mismatches
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C;Species: Mus musculus (house mouse)
                                                                                                 414 GYGYQCIVDHPDFPKPIVRSITK 436
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Best Local Similarity 82.6%;
Matches 19; Conservative
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          Conservative
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Best Local Similarity
Matches 17; Conserv
19;
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          Matches
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Complex: An immunoglobulin C region; immunoglobulin homology (seywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology (fragment) <IMI> F:1-44/Domain: immunoglobulin homology (ims) F:186-254/Domain: immunoglobulin homology <IMI> F:186-254/Domain: immunoglobulin homology <IMI> F:290-361/Domain: immunoglobulin homology <IMI> F:200-361/Domain: immunoglobulin homology <IMI

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R;Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
A;Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain CDNA.
A;Reference number: A02144; MUID:83117774
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C;Species: Mus musculus (house mouse)
C;Decties: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: I68726
R;Shinkal, Y; Makauchi, H; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nu A;Reference number: I544443; MUID:88152907
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C:Species: Mus musculus (house mouse)
C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
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                                                                                                                                     A; Residues: 1-107 arms: A; Residues: 1-107 arms: A; Residues: 1-107 arms: A; Residues: 1-107 arms: A; Cross-references: GB:M22933; NID:g194464; PIDN:AAA37915.1; PID:g194469 C; Superfamily: immunoglobulin C region; immunoglobulin homology cIMM>
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Pred. No. 1.2e-06;
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A;Molecule type: DNA
A;Residues: 1-107 <RES>
                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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82.6%;
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82.68;
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Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserv
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A; Molecule type: mRNA
A; Residues: 1-388 <LIU>
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Best Local Similarity
          A; Accession: 168730
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A; Map position: 14q32.33-14q32.33
A; Introns: 1/1; 104/1; 211/1; 319/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl
F; 22-87/Domain: immunoglobulin homology <IM1>
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J. Biol. Chem. 269, 456-462, 1994
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produ
A;Reference number: A53116; MUID:94103254
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A;Title: Characterization of four novel epsilon chain mRNA and a comparative analysis
A;Reference number: A46536; MUID:93122085
A;Accession: C46536
                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 'GAMTL', 6, 'X', 8-16, 'B', 18-43, 'B', 45-52,55-92,95-97,'B', 99-121,'B',123,'L'
A; Residues: 'GAMTL', 6, 'X', 8-16,'B', 18-43,'B', 45-52,55-92,95-97,'B', 99-121,'B', 123,'L'
A; Experimental source: myeloma protein Nd
B; Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A; Title: Cloning and Sequence determination of the gene for the human immunoglobulin
A; Reference number: A93933; MUID: 83065234
A; Accession: B93933
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A;Title: Purification and characterization of a recombinant human IgE Fc-epsilon frag
A;Reference number: S02438; MUID:88083554
A;Accession: S02438
                                                                                                                   ed., pp
                                A;Note: this sequence difference may be due to polymorphism R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H. in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K.,
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A;Residues: 320-428 <218.
A;Esperimental source: myeloma U266-derived cell line AF-10
A;Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
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A;Molecule type: mRNA
A;Residues: 382-391 <HEZ>
A;Residues: 382-391 <HEZ>
A;Cross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:g263169
A;Experimental source: B cell myeloma 0-266
A;Note: sequence_extracted from NCBI backbone (NCBIP:125299)
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A; Cross-references: GB:S53497; NID:g263162; PIDN:AAB24855.1; PID:g263163
A; Experimental source: B cell myeloma U-266
A; Note: sequence extracted from NCBI backbone (NCBIP:123483)
C; Genetics:
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A; Residues: 1-40;68-114,427-428 <KEN>
A; Cross-references: GB:L00022; NID:g185035
A; Cross-references: GB:J00222; NID:9184755
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A; Residues: 98-352 <IKE>
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                                                                                                                                   R.Sakoyama, Y.; Hong, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A.Title: Nuclectide sequences of immunoglobulin epsilon genes of chimpanzee and oranguta A.Reference number: 136948; MUID:87147196
A.Accession: 136948
A.Stetue: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1.426 < RES>
A.Gross-references: GB:M15398; NID:9176797; PIDN:AAA35416.1; PID:9176798
A.Introns: 103/1; 209/1; 317/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;336-405/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo saptens (man)
C;Species: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C;Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46
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A;Reference number: A23195; MUID:84207910
A;Accession: A23195
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A;Residues: 320-428 <ZHA>
A;Cross-references: EMBL:X63693; GB:S38668; NID:932987
A;Cross-references: EMBL:X63693; GB:S38668; NID:932987
R;Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sugi
Nucleic Acids Res. 11, 719-726, 1983
A;Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha
A;Reference number: A93491; MUID:83168897
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A;Reference number: A22771; MUID:84236029
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R;Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A;Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A;Reference number: A90824; MUID:83001945
A;Accession: A90824
                                Species: Pan troglodytes (chimpanzee)
Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
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A;Residues: 1.428 <FLA>
A;Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
R;Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
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Pred. No. 0.00022;
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R;Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
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epsilon-chain - chimpanzee (fragment)
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Best Local Similarity 65.2%;
Matches 15; Conservative
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                                                                     C;Date: 04-Oct-1996
C;Accession: I36948
R;Sakoyama, Y.; Hong
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C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jan-2000
         class II histocompatibility antigen RT1-D beta-I chain precursor
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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                                                                               experimental
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R;Holowachuk, E.W.; Greer, M.K.
Diabetes 38, 267-271, 1989
A;Title: Unaltered class II histocompatibility antigens and pathogenesis of IDDM in BB
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 15951
R;Robertson, K.A.; McMaster, W.R.
J. Immunol. 135, 4055-4099, 1985
A;Fitle: Complete structure of a rat RTI E-beta chain: Extensive conservation
A;Reference number: 155951; MUID:86060895
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C; Superfamily: class II histocompatibility antigen; immunoglobulin homology F; 137-202/Domain: immunoglobulin homology <IMM>
F;338-407/Domain: immunoglobulin homology <IM4>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;15-105,29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted
F;21.49,99,146,252,275/Bunding alte: carbohydrate (Asn) (covalent) #status
F;121,209/Disulfide bonds: interchain (to heavy chain) #status predicted
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A;Cross-references: GB:M12382; NID:g205437; PIDN:AAA41610.1; PID:g205438
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
F:118-183/Popmain: immunoglobulin homology <!
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C;Date: 17-Apr_1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
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A;Accession: A60497; MUID:89121214
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                      Length 428;
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                                                                                                                                                                    Score 80; DB 1;
Pred. No. 0.00061;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Pred. No. 6.6;
3; Mismatches
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60.9%;
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                                                                                                                                                                    Query Match 55.2
Best Local Similarity 60.9
Matches 14; Conservative
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C; Accession: $10989
R; Syha-Jedelhauser, J.; Reske, K.
Wincleic Acids Res. 18, 4598, 1990
R; Syha-Jedelhauser, J.; Reske, K.
Wincleic Acids Res. 18, 4598, 1990
R; Title: Sequence of rat cDNA clone pLR-beta-112 coding for the RTI.D-beta' chain.
A; Reference number: $10989; MUID: 90356406
A; Accession: $10989
A; Molecule type: mRNA
A; Residues: 1-264 <SYH>
A; Residues: 1-264 <SYH>
A; Residues: 1-1264 <SYH>
A; Residues: 1-1264 <SYH>
A; Residues: 1-264 <SYH>
A; Cross-references: EMBI:X53054; NID: 957169; PIDN:CAA37221.1; PID: 957170
C; Superfamily: class II histocompatibility antigen; immunoglobulin homology
C; Keywords: glycoprotein; heterodimer; transmembrane protein
F; 1-26/Domain: signal sequence #status predicted <SIG>
F; 202/Domain: immunoglobulin homology <IMM>
F; 302/Domain: immunoglobulin homology <IMM>
F; 202/Domain: transmembrane #status predicted <TMM>
F; 209-246/Domain: transmembrane #status predicted <TMM>
F; 46/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: glycoprotein; heterodimer; transmembrane protein
F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 23-345/Product: class I histocompatibility antigen B-F IV alpha chain #status predicted <EXT>
F; 23-310/Domain: extracellular #status predicted <EXT>
F; 111-20/Domain: alpha-1 <EXT1>
F; 111-20/Domain: alpha-2 <EXT2>
F; 214-279/Domain: immunoglobulin homology <IMM>
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A; Cross-references: GB:M31012
B; Culllemot, F.; Billault, A.; Pourquie, O.; Behar, G.; Chausse, A.M.; Zoorob, EMBO J. 7, 2775-2785, 1988
A; Title: A molecular map of the chicken major histocompatibility complex: the cA; Reference number: S01172; MUID:89030642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHC class I histocompatibility antigen B-F IV alpha chain precursor - chicken
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C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999
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A;Residues: 1-345 <GUI>
A;Cross-references: EMBL:X12780; NID:963089; PIDN:CAA31272.1; PID:963090
C;Genetics:
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F;325-345/Domain: intracellular #status predicted <INT>
F;59.107/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;121-183,221-277/Disulfide bonds: #status predicted
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R;Kroemer, G.; Zoorob, R.; Auffray, C.
Immunoapenetics 31, 405-409; 1990
A;Title: Structure and expression of a chicken MHC class I gene.
A;Reference number: A45846; MUID:90316612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 264;
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17;
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Pred. No. 6.6;
3; Mismatches
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Pred. No.
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50.0%;
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195 GEVYTCQVEHPSLPSPV 211
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Gaps

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submitted to the EMBL Data Library, May 1998
A.Description: DNA sequencing and analysis of the chicken major histocompatibility of A.Reference number: 220475
A.Reference number: 220475
A.Accession: T28152
A.Status: preliminary: translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1.355 cML>
A.Residues: 1.355 cML>
A.Resperimental source: clone cB12
C.Gonetics:
A.Genetics:
A.Genetics:
A.Genetics:
A.A.Map position: 16
A.Map position: 16
A.Marcons: 22/1; 110/1; 201/1; 292/1; 339/1; 350/1
C.Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 2; Length 355;
Pred. No. 18;
3; Mismatches 5; Indels
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50.0%;
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271 GDKYQCRVEHASLPQP 286
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Best Local Similarity 50.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                     major histocompatibility complex class I glycoprotein haplotype B21 - chicken C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Saccession: 151309
R; Fulton, J.E.; Thacker, E.L.; Bacon, L.D.; Hunt, H.D.
R; Fulton, J.E.; Thacker, E.L.; Bacon, L.D.; Hunt, H.D.
R; File: Functional analysis of avian class I (BFIV) glycoproteins by epitope tagging an A; Reference number: 151309
A; Reference number: 151309
A; Accession: 151309
A; Accession: 151309
A; Accession: 151309
A; Reference number: 151309
A; Residues: 1-355 cFUL>
A; Coss-references: GB:S78682; NID:g1042200; PIDN:AAB34945.1; PID:g1042201
C; Genetics:
A; Cometics:
A; Cometics
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T28149
MMC class I histocompatibility antigen B-F alpha chain 2 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T28149
R;Milne, S: Kaufman, J: Beck, S.
submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility compl
A;Reference number: 220475
A;Accession: T28149
A;Accession: T28149
A;Accession: T28149
A;Molecule type: DNA
A;Residues: 1-355 AMIL>
A;Molecule type: DNA
A;Residues: 1-355 AMIL>
A;Cross-references: EMBL:AL023516; PIDN:CAA18969.1
A;Cross-references: EMBL:AL023516; PIDN:CAA18969.1
A;Genetics:
A;Gen
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Superfamily: class I histocompatibility antigen; immunoglobulin homology
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Pred. No. 18;
3; Mismatches 5; Indels
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Best Local Similarity 50.0%;
Matches 8; Conservative
          4 |: || ||: | |:| |:| 272 GDKYQCRVEHASLPQP 287
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Matches 8; Conservative
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IgE immunogenic pe Modified MVF Th ep

Run on:

Title:

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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980_DAT:*
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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982_DAT:*
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33.557 Million cell updates/sec
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                                                                                                                                                                                                                                                          August 26, 2002, 10:03:14 ; Search time 82.75 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747574
                                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         747574 seqs, 111073796 residues
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1 CGETYQSRVTHPHLPRALMRSTTKC
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Description	Optimised IgE-CH3 Modified human IqE	Peptide sequence o	Modified MVF Th ep Modified MVF Th ep	Modified MVF Th ep	IqE-CH3 domain ant	Modified HBV surfa	Peptide sequence o
SUMMARIES	AAY79998 AAY91212	AAY68602 AAY80014	AAY91215 AAY91216	AAY68604	AAY80007	AAY91218	AAY68605
ОВ	21 21	21	21	21	21	21	21
a Query Match Length DB	25	25 42	4 4 2 2 2	4 4 2 2	45	45	45
8 Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	140	140 140	140 140	140	140	140	140
Result No.	7	m - ₹	o o	7 8	6	10	11

	14		0.0	4 4	517	AAY91214	Modified MVF Th ep
	15		0.00	46	21	AAY68603	Peptide sequence o
	17		0.00	0 0 0	7 7	AAY80010	igs immunogenic pe Igs immunogenic pe
	18		0.00	9	21	AAY80013	IgE immunogenic pe
	19		0.0	00	21	AAY80015 AAY80008	IGE immunogenic pe
	21		0.0	63	21	AAY80012	IgE immunogenic pe
	22		0.00	63	21	AAX91219	Inv epitope/modifi
	23		0.00	63	27	AAY68606	Peptide sequence o
	25		33.6	106	507	AAY42620	Human IqE Fcepsilo
	26		33.6	110	14	AAR33304	IgE Fc epsilon 3.
	27		33.6	110	14	AAR33314	Variant IgE - muta
	20		9.0	110	14	AAR33318	Variant 19E - muta Variant 19E - muta
	30		33.6	110	14	AAR33319	Variant IGE - muta
	31		33.6	110	14	AAR33320	Variant IgE - muta
	32		33.6	110	14	AAR33321	Variant IgE - muta
	2 2		5.0	110	14	AAK35322	Variant 19E - muta
	35		33.6	110	14	AAR33328	Variant IgE - muta
	36		33.6	110	14	AAR33329	Variant IgE - muta
	37		93.6	110	14	AAR33330	Variant IgE - muta
	300		33.0	110	14	AAR3331 AAR32022	Variant 19E - muta Variant 19E - muta
	40		33.6	110	14	AAR32023	Variant IgE - muta
	41		33.6	110	14	AAR32024	Variant IgE - muta
	4 4 3		9.7	110	14	AAR32025 AAR32026	variant 19E - muta Variant 19E - muta
	. 4. 4.	117	83.6	110	14	AAR32027	Variant IgE - muta
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						ALIGNMENTS	
RES	ULT 1						٠
AAY	AAY79998						
QI X	AAY 79998	ß	tandard;	Peptid	je;	25 AA.	
AC AC	AAY 79998	98;					
xx							
E X	15-MAY	-2000	(first	entry	\sim		
DE	Optimised	Iq	Е-СНЗ Ф	domain	anti	qen peptide for human	IgE.
××	ı	1					
KW	Immuno	mmunoglobul	In E; I	gE; el	Sil	chain; anti	c; antigen;
X X	antibo	immunogenic; antibody: all	ımmuno Pergv:	stimu. aller	rato	<pre>lmmunostimulatory; carrier protein; ne lergy: allergic disease: immunisation: a</pre>	neiper T cell epicope; on: anti-alleraic:
KW	anti-a	naphyl	actic;	anti-a	sth	sthma; anapl	dermati
X e	HOMO	aniens					
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PD	29-DEC	-1999.					
PF	21-JUN-1	-1999;	0M66	99WO-US13959	959.		
PR	20-JUN	-1998;	9805	-0100287	287.		
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antigento peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of Ige, and so preventing triggering and activation of mast cells and basophils and so preventing triggering and activation of mast cells and basophils and downregulation of Ige synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscences Thelper cell epitope (Inottional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigon; HBV; immunogenic; B-cell epitope; lutelnising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic; Plasmodium falciparum; circumsporozoite; antimalarial; CETP; cholestery! ester transport protein; anti-arteriosoleotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                         present invention describes immunoglobulin E (IgE)-CH3 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 140; DB 21;
100.0%; Pred. No. 7.4e-15;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified human IgE CH3 domain, SEQ ID NO:92.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 cgetyqsrvthphlpralmrsttkc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY91212 standard; peptide; 25 AA.
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                 Claim 1; Page 21; 155pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9966957-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
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The invention relates to novel promiseuous T helper cell epitopes (Th), and mannogenic peptides comprising the The pitopes of the invention and mannogenic peptides comprising the The pitopes and peptide immunogens continuing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesteryl ester transport protein (CETP) or HIV epitopes, but more generally against any pathogen, immunoceactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunoceacture self-antigen or tumour antigen. The Th epitopes and peptide immunoceacture protein of peptides or article proteins and publicated immune ceptides or article proteins and publicated immune ceptides or resulting in production of antihodies against a target antigen. Th (tunctional in genetically diverse subjects) into an immunogen peptides. The personnes resulting in production of antihodies against a target antigen. The personnes resulting in production of antihodies against a target of personne proper personne proteins and sequence and proper personnes resulting in production of antihodies against a target of peptides. The personnes antigen peptides and proper peptides and proper personnes are promiseuous of the personne sequence ANY91141 represents a promiseuous T helper peptides. ANY91201 sometostatin and any sequence antigen. ANY91201 represents a promiseuous may be used to promote growth in livestock. ANY91208 is a human Ode CDR2 antiganic peptides which may be used to prevent or treat carteriosic and may be used to promote growth in livestock. ANY91201 represent corpused and may be used to promote growth in an maintie of any personne corpus and may be u
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100.0%; Pred. No. 7.4e-15;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY68602 standard; peptide; 25 AA.
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Matches 25; Conserv
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(UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                         Wang CY, Walfield AM;
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 W09967293-A1
                                                      21-JUN-1999;
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                            29-DEC-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                synthetic helper T cell (Th) epitope and a target antigen, luteinising hormone-releasing hormone (LHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of spermatogenesis, covulation, oestrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper apitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent
                          luteinising hormone-releasing hormone; spermatogenesis; ovulation; osstrus; sexual development; sex hormone; promiscuous T helper epitope; vaccine; contraceptive; hormone-dependent tumour; prostate cancer; breast cancer; endometriosis; boar taint; meat quality; immunocastration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy; disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                   New peptide immunogen containing luteinising hormone-releasing hormone antigen site and helper T cell epitope, for e.g. contraception and treatment of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumours (cancer of prostate or breast, also endometriosis); to prevent boar taint (and improve meat quality) and for immunocastration. The present sequence appears in the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes peptide immunogens comprising a
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100.0%; Pred. No. 7.4e-15;
ive 0; Mismatches 0;
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             Helper T cell epitope; peptide immunogen; LHRH;
                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 92; 102pp; English
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                                                                                                                                                                                                                                     (UNBI-) UNITED BIOMEDICAL INC.
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Matches 25; Conserv
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                                                                                             Unidentifled
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antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of 1gE, and so preventing triggering and activation of mast cells and basophils and downregulation of 1gE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against 1gE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermattis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AA77994 to AA80084 represent amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatcostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic; Plasmodium falciparum; circumsporozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.
New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy \,\text{-}\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                       present invention describes immunoglobulin E (IgE)-CH3 domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 42;
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                                                                                Claim 14; Page 76; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY91215 standard; peptide; 42 AA.
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Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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98US-0100412. 99WO-US13975

New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus (UNBI-) UNITED BIOMEDICAL INC. WPI; 2000-160564/14. 21-JUN-1999; 20-JUN-1998; Wang CY;

The invention relates to novel promiscuous T helper cell epitopes (Th),
and immunogenic peptides comprising the Th epitopes of the invention
cc and immunogenic peptides comprising the Th epitopes of the invention
cc along with B cell epitopes. The The pitopes and peptide immunogens
containing them, are used to induce a Thelper cell response,
containing them, are used to induce a Thelper cell response,
cc specifically against Plasmodium falciparum, cholesteryl ester transport
cc protein (CETP) or HIV epitopes, but more generally against any pathogen,
immunoractive self-antigen or tumour antigen. The Th epitopes and
cell family period or tumour antigen. The Th epitopes and
continuous infections (HIV) foot-and-mouth disease or malaria); for cancer
continuous transport of inhibition of the action of luteinising hormone
creleasing hormone (LHRH) for contraception, treatment of hormonecreleasing hormone (LHRH) for contraception, treatment of hormonecreleasing hormone (LHRH) for contraception, treatment of hormonecc releasing hormone (LHRH) for contraception, treatment of hormonecc dependent cancer, prevention of boar taint in meat, and
immunocastration); for promoting the growth of animals; or for
treating allergies or arteriosclerosis. Incorporation of a promiscuous
creaponse, resulting in production of antibodies against a target
creaponse, resulting in production of antibodies against a target
creaponse, resulting in production of antibodies against a target
creaponse, resulting in production of antibodies against a target
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creaponse, resulting in production of antibodies against a target
creaponse, resulting in production of antibodies against a target
creaponse, resulting in produc peptides comprising sometostatin and a Th epitope. Sometostatin finding man be used to promote growth in livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AAY90212 is a modified version of a human IgE amingobulin E) CH3 Gomain, and AAY90213.Y90219 are Th epitope/IgE CH3 antigenic peptides which may be used in the treatment of allergies. AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) VPI capsid profein and AAY9121-Y91122 comprise this peptide and a The epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS antigen and an WF The epitope and may be used in a malaria vaccine. AAY91228-Y9131 represent CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a cETP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257 AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAA91198 and AAY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and Example 6; Page 98-99; 129pp; English.

42 AA; Sequence Score 140; DB 21; Length 42; Pred. No. 1.3e-14; 100.0%; 100.0%; Best Local Similarity Query Match

ó Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigon; HBV; immunopelnc; B coell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoplobulin B; IgB; anti-allergic; Plasmodium falciparum; circumsporozotie; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic. Gaps ö Indels Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:96. ö Mismatches 42 AAY91216 standard; peptide; 42 AA. 25 .; 0 18 cgetygsrvthphlpralmrsttkc 1 CGETYQSRVTHPHLPRALMRSTTKC (UNBI-) UNITED BIOMEDICAL INC 99WO-US13975. 98US-0100412. (first entry) Chimeric - Measles virus. Chimeric - Homo sapiens. Conservative WO9966957-A2. 21-JUN-1999; 20-JUN-1998; 22-MAY-2000 29-DEC-1999. 25; AAY91216; 9 Matches AAY91216 RESULT oy O g

WPI; 2000-160564/14. Wang CY;

New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus

Example 6; Page 99; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesteryl ester transport protein (CETP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Thepitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of luteinising hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration); for promoting the growth of animals; or for treatment of hormone immunocastration); for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous in proves capacity to induce a strong T helper cell-mediated immune improves capacity to induce a strong T helper cell-mediated immune improves capacity to induce a strong T helper cell-mediated immune improves capacity to induce a strong T helper cell-mediated immune improves capacity to induce a strong T helper cell-mediated immune improves capacity to induce a strong T helper cell-mediated immune improves capacity to induce a strong T helper cell-mediated immune improves capacity to induce a strong T helper cell-mediated immune improves capacity to induce a strong T helper cell-mediated immune improves capacity to induce of antibodies against a target capacity to induce of antibodies against a target capacity capacity to induce a strong T helper cell-mediated immune improves the capacity to induce a strong T helper cell-mediated immune improves the capacity to induce a strong T helper cell-mediated immune improves the capacity to induce a strong T helper cell-mediated immune improves capacity to induce of antibodies against a ta antigen. The tan replace carrier proteins and pathogen-derived T helper epitopes. Sequence AAY91121 represents a promiscuous T helper epitope from the measles virus F (MVF) protein and sequences AAY91122-Y91142.

AAY91226 and AAY91246 represent synthetic Th epitopes based on the MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope MAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.

AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides

antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus New artificial T helper cell epitope and derived immunogens with target

Example 6; Page 99; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens

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comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197

1s the LHRH target antigenic peptide used in these LHRH antigenic

peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic

peptides comprising somatostatin and a Th epitope. Somatostatin

Immunogens may be used to promote growth in livestock. AAY91208 is a

human CD4 CDR2-like domain antigenic site, and AAY91209-Y99211 are MVH Th

epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV

infection of T cells. AAY90212 is a modified version of a human IgE

ontigenic peptides which may be used in the treatment of allergies.

AAY91220 is a peptide derived from foot and mouth disease virus (FMBV)

VPI capsid protein and AAY91221-Y91222 comprise this peptide and a Th

epitope. AAY91221 is a Plasmodium falciparum circumsporozoite (CS) target

antigen, and AAY91224-Y91255 comprise the CS antigen and an WNF Th

cepitope and may be used in a malaria vaccine. AAY91289-Y91231 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a crep-derived peptides and AAY91241 are immunogens comprising a retriosclerosis and cardiovascular disease. AAAy9124 and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising WVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAX91198 and AAX91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the
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Ouery Match 100. Best Local Similarity 100. Matches 25; Conservative

25 42 18 cgetygsrvthphlpralmrsttkc 1 CGETYQSRVTHPHLPRALMRSTTKC a ö

AAY91217 standard; peptide; 42 AA. (first entry) 22-MAY-2000 AAY91217;

Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:97.

Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigon; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin B; IgE; anti-allergic; eholesteryl ester transport protein; anti-altergic; cholesteryl ester transport protein; anti-arteriosclerotic.

Chimeric - Measles virus. Chimeric - Homo sapiens.

W09966957-A2

29-DEC-1999

99WO-US13975 21-JUN-1999;

(UNBI-) UNITED BIOMEDICAL INC 98US-0100412 20-JUN-1998;

Wang CY;

WPI; 2000-160564/14.

containing them, are used to Induces a Thelper cell response, specifically against Plasmodium falciparum, cholesteryle ster transport proficioning them, are used to Induce a Thelper cell response, specifically against Plasmodium falciparum, cholesteryle ster transport protein (CETP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The The pitopes and peptide immunogens may be used for prevention of the action of Intenising hormone content infections (HIV, foot-and-mouth disease or malaria); for cancer immunoreactive self-antigen or the action of Intenising hormone celeasing hormone (HRH) foot-and-mouth disease or malaria); for cancer immunosertation); for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous celeasing allergies or arteriosclerosis. Incorporation of a promiscuous of furcating allergies or arteriosclerosis. Incorporation of a promiscuous improves capacity to induce a strong Thelper cell-mediated immune response, resulting in production of antibodies against a target antigen. The nor replace carrier proteins and pathogen derived Thelper ceptiopes. Sequence AAY91141 represents a promiscuous Thelper from the measales vivus [HWY) surface antigen; and sequences. Sequence AAY91145 represents a promiscuous Theptope. AAY91155 and SAY91154. Tepresents a promiscuous The epitope. AAY91197 or pathogen. Sequence AAY91141 represents a promiscuous The epitope. AAY91197 or pathogen. Sequence AAY91144 replace of comprising an LHH sequence of order of a promiscuous The epitope. AAY91197 or peptides. AAY91105, AAY9127 and AAY91245 replace of the peptides comprise in a malacet comprise the comprise of promite growth in livestock. AAY91209 reptides which may be used to promise the centum of a cells. AAY90212 reptides which may be used in the treatment of a limentogen may be used to promise the C immunoglobulin By CH3 domain and the present of cells. AAY90122 reptides which may be used to prevent HIV ceptio arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. Axy1108 and AxY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention

42 AA; Sequence

Gaps ö Length 42; Indels 100.0%; Score 140; DB 21; 100.0%; Pred. No. 1.3e-14; iive 0; Mismatches 0; 25 1 CGETYQSRVTHPHLPRALMRSTTKC 25; Conservative Sest Local Similarity Query Match Matches

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18 cgetygsrvthphlpralmrsttkc

ŏ ga AAY68604 ID AAY68

AAY68604 standard; peptide; 42 AA

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Gaps

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Indels

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WPI; 2000-160562/14.
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AAY68604;
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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disnified bridge) to stabilise conformational in genetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobulinitatory; carrier protein; helper T cell epitope; antibody; allergic disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy {\,}^{\circ}
                                                                                                                                                                                                                                                                                                                                                                        IgE-CH3 domain antigen peptide antigenic site 15b SEQ ID NO:14.
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Pred. No. 1.5e-14;
Mismatches 0;
Pred. No. 1.3e-14;
Mismatches 0;
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       Best Local Similarity
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                                     Helper T cell epitope; peptide immunogen; LHRH;
luteinising hormone-releasing hormone; spermatogenesis; ovulation;
osetrus; sexual development; sex hormone; promiscuous T helper epitope;
vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
breast cancer; endometriosis; boar taint; meat quality; immunocastration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes peptide immunogens comprising a synthetic helper T cell (Th) epitope and a target antigen, luteinising hormone-releasing hormone (LHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, oestrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and immunogens of the invention are used to vaccinate against mammaliae for use as (reversible) contraceptive; control of hormone-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide immunogen containing luteinising hormone-releasing hormone antigen site and helper {\tt T} cell epitope, for e.g. contraception and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumours (cancer of prostate or breast, also endometriosis); to prevent boar taint (and improve meat quality) and for immunocastration. The present sequence appears in the specification.
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                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                            Peptide seguence of the invention.
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                                                  (first entry)
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AA;

42

Query Match

Length 45;

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hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FWDV; foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic; Plasmodium falciparum; circumsporozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                     New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis
                                                                                                       Promiscuous T-cell epitope; measles virus F protein; MVF;
                                                                                  Modified HBV surface Ag/IgE CH3 domain, SEQ ID NO:98.
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                   AAY91218 standard; peptide; 45 AA.
                                                                                                                                                                                                                                                                                                                                                                                antigenic site, for immunization
or human immune deficiency virus
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                                                                                                                                                                                       Chimeric - Hepatitis B virus.
Chimeric - Homo sapiens.
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                                         AAY91218;
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RESULT 10
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c pitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
c infection of T cells. AAY90212 is a modified version of a human IgE
(immunoglobulin B) CH3 domain, and AAY90213-Y90219 are Thepitope/IgE CH3
antigenic peptides which may be used in the treatment of allergies.
AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
vPl capsid protein and AAY91221-Y91222 comprise this peptide and a Th
c epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
c epitope and may be used in a malaria vaccine. AAY91224-Y91231 represent
CCTP-derived peptides and AAY9123-Y91241 are immunogens comprising a
CETP peptide and a Th epitope which may be used to prevent or treat
arterioscierosis and cardiovascular disease. AAY9124-Y91251 and AAY91257
are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91256
AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
CC Epitope which may be used as a component in an anti-HIV-1 vaccine.
AAY91198 and AAY91199 are respectively an immunostimulatory invasin
C protein epitope from Yersinia species, and hinge spacer peptide, both of
c protein epitope from Yersinia species, and hinge spacer peptide, both of
c protein may optionally be used in the antigenic peptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helper T cell epitope; peptide immunogen; LHRH;
luteinising hormone-releasing hormone; spermatogenesis; ovulation;
osetrus; sexual development; sex hormone; promiscuous T helper epitope;
vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
breast cancer; endometriosis; boar taint; meat quality; immunocastration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes peptide immunogens comprising a synthetic helper T cell (Th) epitope and a target antigen, luteinising hormone-releasing hormone (LHRH). The peptide immunogens cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 140; DB 21;
100.0%; Pred. No. 1.5e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 95; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY68605 standard; peptide; 45 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CGETYQSRVTHPHLPRALMRSTTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0100414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-160562/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09966952-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang CY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from hepatitis B virus (HBV) surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope. AAY9124-Y91195 are synthetic epitopes derived from this HBV epitope. AAY91257 and AAY91242-Y91244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin a the MAY Epitope. Somatostatin and a Th epitope.
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Gaps

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Length 45; Indels constraints (disulfide bridge) to stabilise conformational features and

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                 regulation of spermatogenesis, ovulation, oestrus, sexual development and secrettion of sex hormones. Provision of a promiscousor Thelper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and immunogens of the invention are used to vaccinate against the peptide. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast, also endometriosis); to prevent boar taint (and improve meat quality) and for immunocastration. The present sequence appears in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigenic peptides (I). (I) have anti-allegic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (Anctional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobelic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylactic; anti-asthmatic; asthma; anaphylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                        Gaps
  induction of a specific immune response to LHRH which is involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes immunoglobulin E (IgE)-CH3 domain
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                                                                                                                                                                                                                                                                                                               Length 45;
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                                                                                                                                                                                                                                                                                                           100.0%; Score 140; DB 21;
100.0%; Pred. No. 1.5e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IgE immunogenic peptide conjugate SEQ ID NO:18.
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                                                                                                                                                                                                                                                                                                                                                                                                                      21 cgetygsrvthphlpralmrsttkc 45
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                                                                                                                                                                                                                                                                                                                                                                                               1 CGETYQSRVTHPHLPRALMRSTTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY80011 standard; Peptide; 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNBI-) UNITED BIOMEDICAL INC
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Matches 25; Conservative
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                                                                                                                                                                                                                                                   45 AA;
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                                                                                                                                                                                                                                                     Sequence
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The invention relates to novel promiscuous T helper cell epitopes (Th),
and immunogenic peptides comprising the Th epitopes of the invention
along with B cell epitopes. The Th epitopes and peptide immunogens
containing them, are used to induce a T helper cell response,
specifically against Plasmodium falciparum, cholesteryl ester transport
protein (EEFP) or HIV epitopes, but more generally against any pathogen,
immunoreactive self-antigen or tumour antigen. The Th epitopes and
peptide immunogens may be used for prevention and/or treatment of
infections (HIV, foot-and-mouth disease or malaria); for cancer
infections (HIV) foot-and-mouth disease or malaria); for cancer
cleasing hormone (LHRH) for contraception, treatment of hormone
cleasing hormone (LHRH) for contraception, treatment of hormone
dependent cancer, prevention of boar taint in meat, and
immunocastration); for promoting the growth of animals; or for
treating allergies or arteriosclerosis. Incorporation of a promiscuous
Th (functional in genetically diverse subjects) into an immunogen
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                maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic; plasmodium falciparum, circumsporozoite; antimalarial; CETP; cholestery! ester transport protein; anti-arteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arterlosclerosis
                                                                                                                                                                                             Gaps
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                                                                                                                                                        Length 46;
                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:93.
                                                                                                                                                    Score 140; DB 21;
Pred. No. 1.5e-14;
Mismatches 0;
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                                                                                                                                                                                                                                                      22 cgetygsrvthphlpralmrsttkc 46
                                                                                                                                                                                                                                 1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or human immune deficiency virus
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                                                                                                                                                                                                                                                                                                                                                                        AAY91213 standard; peptide; 46
                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Measles virus.
Chimeric - Homo sapiens.
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-160564/14.
                                                                                                                                                                      Best Local Similarity
Matches 25; Conserv
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                                                                                             46
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                                                                                               Sequence
                                                                                                                                                        Query Match
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cresponse, resulting in production of antibodies against a target antigen. The can replace carrier proteins and pathogen-derived Theiper antigen. The can replace carrier proteins and pathogen-derived Theiper epitopes. Sequence AXY91121 represents a promiscuous Theiper epitope (CC from the measles virus F (MVP) protein and sequences AXY91122-791142, AXY91226 and AXY91245 represents a promiscuous Theiptopes based on the from theipertitis B virus (fibW) surface antigen, and sequences AXY91122-791144.

AXY9126-Y91196, AXY91227 and AXY91242-Y91344 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AXY91197 and AXY91242-Y91344 are antigenic peptides comprising somatostatin, and AXY91201-Y92107 are antigenic peptides comprising somatostatin, and AXY91201-Y92107 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin compress may be used to promote growth in livestock. AXY91201 are antigenic peptides comprising somatostatin antigenic site, and AXY91201-Y90201 are myll the comprising somatostatin antigenic site, and AXY91201-Y90201 are myll the comprising peptides which may be used to promote growth in livestock. AXY91208 is a modified version of a lumman IQU cope. Comprising which may be used in the treatment of allergies. AXY91201 is a peptide derived from foot and AXY91219 are The epitope. IX of antigenic peptides which may be used in the treatment of allergies. The copitope and may be used in malaria vaccine. AXY91228 roughlish and AXY91221 and AXY91222 roughlish and may be used in an allaria vaccine. AXY91228 roughlish and AXY91221 and AXY91228 roughlish and may be used in an anti-HIV-1 waccine. AXY9128-Y91231 are antigenic peptides and and AXY91222 roughlish and AXY91231 are antigenic peptides comprising WWH Th and HIV-1 heutralishing a cell epitopes, and AXY91228 roughlish and AXY9128-Y9123 are antigenic peptides comprising WHY Th and AXY9129 are antigenic peptides comprisely and AXY9128-Y9123 are antigenic peptides. AXY9128-Y9123 are antigenic peptides wh
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46 AA; Seguence

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                              Gaps
                              0
    Length 46;
                            Indels
100.0%; Score 140; DB 21;
100.0%; Pred. No. 1.5e-14;
Live 0; Mismatches 0;
                           Conservative
Ouery Match
Best Local Similarity
Matches 25; Conserv
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AAY91214 standard; peptide; 46 AA. AAY91214

RESULT 14

AAY91214;

(first entry) 22-MAY-2000

Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:94.

Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin B; IgB; anti-allergic; plasmodium falciparum; circumsporozoite; antimalarial; CEFP; cholesteryl ester transport protein; anti-arteriosclerotic.

Chimeric - Measles virus. Chimeric - Homo sapiens.

W09966957-A2.

29-DEC-1999.

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The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogenic peptides comprising the peptides and peptide immunogenic peptides. The The peltopes and peptide immunogenic peptides. The The peltopes and peptide immunogenic peptides are used to induce a T helper cell response, and centaring them, are used to induce a T helper cell response, or peptide immunogenic peptide immunogenic may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of lutehising hormone cell assign phormone (LIRH) for contraception, treatment of hormone-cell and phormone (LIRH) for contraception, treatment of hormone-cell and performed promone contraception of boar taint in meat, and a promiscuous of immunocastration); for promoting the growth of animals or for immunocastration; for promoting the growth of animals or for immunocastration; for promoting the growth of animals or for immunocastration; for promoting the growth of animals or for immunocastration; for promoting the growth of animals or for immunocastration; for promoting the growth of animals or for immunocastration; for promoting the growth of animals or for immunocastration; for interesting in genetically diverse subjects) into an immunogen cell proper cepticopes. Sequence AAV91121 represents a promiscuous T helper cell redarged immunocastration; and AAV91226 and AAV9126 represents a promiscuous T helper cell redarged into percent in the treatment of anitype. AAV91197 are anitypen. AAV91197 and AAV91126 and AAV9126. AAV91120 and AAV91201-V9120 are anitypenic peptides. AAV91201-V9120 and AAV91201-V9120 and AAV91201-V9120 anitypenic peptides any periode comprising an LHRH sequence joined to a promiscuous The proper anitypenic peptides anitypenic peptides and AAV91201-V9120 and AAV91201-V9120 animunocast anitypenic peptides and AAV91201-V91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory invasin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the
                                                                                                                                                                                                                New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus
                                                                                                                                                                                                                                                                                                  Example 6; Page 98; 129pp; English.
                                                                                   (UNBI-) UNITED BIOMEDICAL INC
  99WO-US13975.
                                             98US-0100412.
                                                                                                                                                                     WPI; 2000-160564/14.
                                             20-JUN-1998;
21-JUN-1999;
                                                                                                                            Wang CY;
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46 AA; Sequence

Gaps ; 0 Length 46; Indels 100.0%; Score 140; DB 21; 100.0%; Pred. No. 1.5e-14; tive 0; Mismatches 0; Conservative Query Match Best Local Similarity Matches 25; Conserv

46 AA;

Sequence

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The specification describes peptide immunogens comprising a synthetic helper T cell (Th) epitope and a target antigen, luteinising hormone-releasing hormone (LHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, oestrus, sexual development and secretion of sex hormones. Provision of a promiscous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast, also endometriosis); to prevent beast taint (and improve meat quality) and for immunocastration. The present sequence appears in the specification.
                                                                                                                                                                                                                                           Helper T cell epitope; peptide immunogen; LHRH;
luteinising hormone-releasing hormone; spermatogenesis; ovulation;
osstrus; sexual development; sex hormone; promiscuous T helper epitope;
vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
breast cancer; endometriosis; boar taint; meat quality; immunocastration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide immunogen containing luteinising hormone-releasing hormone antigen site and helper {\tt T} cell epitope, for e.g. contraception and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 93; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                            Peptide sequence of the invention.
25
             22 cgetygsrvthphlpralmrsttkc 46
                                                                                                              AAY68603 standard; peptide; 46 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label- Gly, Thr
                                                                                                                                                                                                                                                                                                                                                                                                            /label= Ser, Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                          label- Lys, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label- His, Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label- Lys, Arg
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1 CGETYQSRVTHPHLPRALMRSTTKC
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Gaps
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0
 Length 46;
                     Indels
Score 140; DB 21;
Pred. No. 1.5e-14;
Mismatches 0;
                                       25
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                                                   cgetygsrvthphlpralmrsttkc
                                        1 CGETYQSRVTHPHLPRALMRSTTKC
 100.0%;
100.0%;
                      Conservative
  Query Match
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Matches 25; Conserv
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Search completed: August 26, 2002, 10:07:01 Job time: 227 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 26, 2002, 10:03:14 ; Search time 45.87 Seconds (without alignments) 52.370 Million cell updates/sec

US-09-701-623C-5

CGETYQSRVTHPHLPRALMRSTTKC 25 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Ig epsilon chain classes epsilon chain creceptor shypothetical protein lasses epsilon chain conserved in conserved epsilon chain myosin heavy chain coll cycle protein conserved hypothetical conserved experience.	
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154421	A03859	876316	155951	A60497	S10989	T32334	T21355	н87906	MWRBCB	148153	A37102	806006	A59286	138055	JX0178
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93	106	210	245	264	264	343	573	676	1038	1934	1935	1935	1935	1937	1938
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	5	45	45	45	45	45	45	45	45	45	45	45	45	45	45
45	`														

ALIGNMENTS

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psilon heavy chain constant region g
                                                                   33 #text_change 16-Jul-1999
324; A94418; B93933; S02438; A53116;
                                                                                                                                                                                                                                55; NID:9185035
Honjo, T.
                                  Ig epsilon chain C region - human
                                                 C;Species: Homo sapiens (man)
C;Date: 31-Mar
                                                                                                                                                                                           A; Molecule type
A; Residues: 1-4
A; Cross-referen
R; Ueda, S.; Nak;
EMBO J. 1, 1539
                                                                                                                                                                                                                                                                                     A; Title: Long te
                                                                                                                                                                                                                                                                                                     A; Reference num
                                                                                                                                      A; Reference num
                                                                                                                                                                            A; Accession: A2
                                                                                                     R; Flanagan, J.(
EMBO J. 1, 655
                                                                                        C; Accession: A:
RESULT
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a human immunoglobulin epsilon pseu

A; Accession: A23

A; Rolecule type: __und A; Residues: 2-428 <UED> A; Residues: 2-428 <UED> A; Cross-references: GBL J00222; NID:g184755 B; Zhang, K.; Saxon, A.; Max, E.E. J. Exp. Med. 176, 233-243, 1992 A; Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splic A; Reference number: PH1214; MUID:92308839 A; Accession: PH1214

A; Molecule type: DNA
A; Residues: 320-428 < CHA>
A; Cross-references: EMBL:X63693; GB:S38668; NID:g32987
B; Seno, M.; Kurokawa, T.; Ondo, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; S Nucleic Acids Res. 11, 719-726, 1983
A; Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon A; Reference number: A93491; MUID:83168897
A; Residues: 1-428 < CENDA; Residues: 1-429 < CENDA; Residues: 1-429 < CENDA; Residues: 1-428 < CEN

A; Molecule type: DNA

A; Residues: 1-358, 'L',360-428 < MAX>
A; Ross-references: GB:J00222; NID:9184755
A; Cross-reference difference may be due to polymorphism
A; Note: this sequence difference may be due to polymorphism
B; Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
A; Reference number: A94418
A; Reference number: A94418
A; Molecule type: protein

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Gaps

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C. Species: Rattus norvegicus (Norway rat)

C. Saccession: 493442; A90937; A02143

R. Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.

Nucleic Acids Res. 10, 6041-6049, 1982

R. Fitle: Structure and evolution of the heavy chain from rat immunoglobulin E.

A. Feference number: A93442; MUID:83064537

A. Molecule type: mRNA

A. Residues: 1-429 cHEL>

A. Molecule type: mRNA

A. Residues: 1-429 cHEL>

R. Kindsvogel, W. R.; Reddy, E. P.; Moore, J. M.; Faust Jr., C. H.

DNA 1, 335-343, 1982

A. Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction A. Reference number: A90937

A. Molecule type: mRNA

A. Reference number: A90937

A. Molecule type: mRNA

A. Reference number: A90937

A. Molecule type: mRNA

A. Residues: MNA

A. Res
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C; Species: Pan troglodytes (chimpence)
C; Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C; Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C; Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C; Sakoyama, Y:; Hong, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A; Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orang
A; Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orang
A; Accession: 136948
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-426 CRES
A; Residues: 1-426 CRES
A; Cross-references: GB:M15398; NID:g176797; PIDN:AAA35416.1; PID:g176798
C; Genetics:
C; Genetics:
A; Introns: 103/1; 209/1; 317/1
C; Superfamily: immunoglobulin C region; immunoglobulin homology
F; 336-405/Domain: immunoglobulin homology < IMM>
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Fi223-291/Domain: immunoglobulin homology <IM3>
Fi327-398/Domain: immunoglobulin homology <IM4>
Fi46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predi
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Pred. No. 2.3e-09;
1; Mismatches 1;
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Pred. No. 0.00024;
                 Pred. No. 5.8e-10;
                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig epsilon-chain - chimpanzee (fragment)
                                                                                                                                                                                                                                           294 GETYQCRVTHPHLPRALMRSTTK 316
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                                                                                                                                                                                      2 GETYQSRVTHPHLPRALMRSTTK
     95.78;
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Local Similarity 91.3%;
nes 21; Conservative
                                                                      22; Conservative
           Best Local Similarity
Matches 22; Conserv
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A; Status: nucleic acid sequence not shown
A; Macule type: mRNA
A; Residues: 98-352 < LKE>
R; Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
J. Biol. Chem. 269, 456-462, 1994
A; Attle: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A; Reference number: A53116, MUID:94103254
A; Reference number: A53116
A; Residues: 320-428 < LHE
A; Residues: 320-428 < LHE
A; Residues: 320-428 < LHE
A; Residues: Sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
B; Hellman, L.
B; H
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A;Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of A;Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of A;Reference number: A46536; MUID:93122085

A;Reference number: A6536; MUID:93122085

A;Ression: C46536

A;Restius: preliminary: not compared with conceptual translation

A;Molecule type: mRNA

A;Restius: preliminary: not compared with conceptual translation

A;Restius: G8:55273; NID:9263166; PIDN:AAB24857.1; PID:9263167

A;Cross-references: B cell myeloma U-266

A;Note: sequence extracted from NCBI backbone (NCBIP:125297)
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A;Cross-references: GDB:119335; OMIM:147180
A;Cross-references: GDB:119335; OMIM:147180
A;Cross-references: GDB:119335; OMIM:147180
A;Cross-references: GDB:119335; OMIM:147180
A;Cross-references: 14432.31443.3193
A;Introns: 1/1: 104/1; 211/1; 313/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapped family: immunoglobulin cequion; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology cima;
F;128-195/Domain: immunoglobulin homology cima;
F;328-301/Domain: immunoglobulin homology cima;
F;384-407/Domain: immunoglobulin homology cima;
F;386-407/Domain: immunoglobulin homology cima;
F;147baulfide bonds: interchain (to light chain) #status predicted
F;15-105,29-85,135-133,239-299,345-405/Disulfide bonds: #status predicted
F;11,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;11,20,20/Bisulfide bonds: Interchain (to heavy chain) #status predicted
A, Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',12
A, Experimental source: myeloma protein Nd
R; Kenten, J.H.; Molgard, H.V; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
Proc. Nall. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A, Title: Cloning and sequence determination of the gene for the human immunoglobulin eps
A, Reference number: A93933; MUID:83065234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of a recombinant human IgE Fc-epsilon fragmen
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A.Status: preliminary; not compared with conceptual translation
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: DNA
A.Residues: 401-428 <HE3>
A.Cross-references: GB:S53497; NID:g263162; PIDN:AAB24855.1; PID:g263163
A.Experimental source: B cell myeloma U-266
A.Note: sequence extracted from NCBI backbone (NCBIP:123483)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: D46536
A,Status: preliminary; not compared with conceptual translation
A;Status: preliminary
A;Status: mRNA
A;Residues: 382-391 <HE2>
A;Cross-references: G8:55276; NID:9263168; PIDN:AAB24858.1; PID:9263169
A;Experimental source: B cell myeloma U-266
A;Note: sequence extracted from NCBI backbone (NCBIP:125299)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Ikeyama, S.
FEBS Lett. 224, 306-310, 1987
A;Title: Purification and characterization
A;Reference number: S02438; MUID:88083554
A;Accession: S02438
                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-40; 68-114;427-428 <KEN>
A;Cross-references: GB:L00022; NID:g185035
R; Ikeyama, S.
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Gaps

: 0

Length 429;

57.1%; 60.9%;

Query Match Best Local Similarity

Score 117; DB 1; Length 428

83.68;

Query March

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A residues: 1-388 <a href="Line">Line</a>
A residues: 1 PID:9387220
C remplex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IqA and IgM, the subunits associate into creation; immunoglobulin homology and Immunoglobulin homology (fragment) rimmunoglobulin homology (imagent) rimmunoglobulin rimmunoglobulin homology (imagent) rimmunoglobulin 
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C; Species: Ginglymostoma cirratum (nurse shark)
C; Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jul-2000
C; Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jul-2000
C; Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change E.C.; Flajnik, M.F.
Nature 374, 168-173, 1995
A; Title: A new antigen receptor gene family that undergoes rearrangement and extensiv A; Reference number: $60266; MUID: 95183140
A; Accession: $60266
A; Status: preliminary; nucleic acid sequence not shown
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C;Accession: S38864
R;Kipp, B.; Becker, W.; Schlaak, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:227397; NID:g416537; PIDN:CAA81788.1; PID:g940782 C;Superfamily: immunoglobulin C region; immunoglobulin homology F;353-421/Domain: immunoglobulin homology <IMM>
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A; Description: Combination of a defined specificity
A; Reference number: S38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 2;
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 1;
Pred. No. 0.98;
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Pred. No. 1.4;
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A; Molecule type: mRNA
A; Residues: 1-548 <KIP>
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       A; Accession: A02144
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: 168726
R; Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A; Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid a A; Reference number: 154443; MUID:88152907
A; Accession: 168726
A; Accession: 168726
A; Molecule type: DNA
A; Molecule type: DNA
A; Mesidues: 1-107 < REES.
A; Residues: 1-107 < REES.
A; Cross references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460
C; Superfamily: immunoglobulin C region; immunoglobulin homology < IMM>
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Pred. No. 0.26;
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Pred. No. 0.26;
3; Mismatches
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                                                                       2 GETYQSRVTHPHLPRALMRSTTK 24
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National receptor substrate ppl85
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus
S1648
R; Sun, X.J.; Rothenberg, P.; Kahn, C.R.; Backer, J.M.; Araki, E.; Wilden, P.A.; Cahill
R; Sun, X.J.; Rothenberg, P. Structure of the insulin receptor substrate IRS-1 defines a unique signal tr
A; Reference number: S16948; MUID:91287824
A; Reference number: S16948; MUID:91287824
A; Residues: 1-1235 csUN
A; Residues: 1-1235 csUN
A; Residues: 1-1235 csUN
A; Residues: P.L.; Lane, W.S.; Karasik, A.; Backer, J.; White, M.; Kahn, C.R.
J. Biol. Cham. 266, 8302-8311, 1991
A; Title: Purification and partial sequence analysis of ppl85, the major cellular subs
A; Reference number: A39811; MUID:91217066
A; Molecule type: protein
A; Molecule type: protein and the beta chain of the insulin receptor itself are the major comment: This protein in response to insulin is maximal at 30 8e
                                                                                                                                                                     N; Contains: 122K protein
C; Species: tobacco mosaic virus, TMV
A; Variety: strain Cr-TMV
C; Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 20-Sep-1999
C; Accession: S46699; S48659
R; Dorokhov, Y.L.; Ivanov, P.A.; Novikov, V.K.; Agranovsky, A.A.; Morozov, S.Y.; Efimo
FEBS Lett. 350, 5-8
                                                                                                                                                                                                                                                                                                                                                                                                                       genome organization of a tobamovirus infect
                                                                                                                                                                                                                                                                                                                                                                                                            A:Title: Complete nucleotide sequence and genome organization of a tobamovirus infect A:Reference number: $48659; MUID:94341372
A:Reference number: $48659; MUID:94341372
A:Reference number: $48659; MUID:94341372
A:Rolecule type: genomic RNA
A:Residues: 1-1601 < DOR>
A:Rolecule type: genomic RNA
A:Residues: 1-1601 < DOR>
A:Cross-references: EMBL:229370; NID:9488713; PIDN:CAA82559.1; PID:9619908
A:Experimental source: tobamovirus infecting cruciferae plants (cr-TMV)
A:Rote: readthrough of the terminator UGA occurs between codons CAA for 1107-Gln and A:Note: the internal stop codon is translated as X
C:Superfamily: cucumber mosaic virus RNA | protein
F:1-1601/Product: 178K protein #status predicted <PRO2>
F:1-1107/Product: 122K protein #status predicted <PRO1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 2; Length 1601;
Pred. No. 35;
4; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.4%; Score 49.5; DB 1;
47.8%; Pred. No. 32;
Live 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                      178K protein - tobacco mosaic virus (strain cr-TMV)
N;Alternate names: readthrough protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GETYQS----RVT------HPHLPRALMRSTTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insulin receptor substrate IRS-1 - rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 35.7%;
Best Local Similarity 36.8%;
Matches 14; Conservative ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 11; Conserv
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A:Title: Nuclectide sequence of Chinese rape mosaic virus (cilseed rape mosaic virus), a A; Exterence number: 856053; MuID:96197410
A; Accession: 856053
A; Status: nucleic acid sequence not shown; translation not shown
A; Residues: 1-1597 (AGT)
A; Residues: 1-1597 (AGT)
A; Cross-references: EMBL:U3094
A; Note: readthrough of the terminator UGA occurs between codons CAA for 1103-Gln and CAA
A; Note: the internal stop codon is translated as X
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995
C; Superfamily: cucumber mosaic virus RNA 1 protein
C; Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                      Chacesion: C8648
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; LJ, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Southwick, A.M.; Sun, H.; Tallon, A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: AE005172; NID: 98671838; PIDN: AAF78401.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome polyprotein - Chinese rape mosaic virus
N;Alternate names: RNA replicase
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: Chinese rape mosaic virus
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 17-Mar-1999
C;Accession: S65053
                                                                                                                                                                                                                                                                            C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
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Pred. No. 35;
4; Mismatches 6; Indels ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 320;
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                                                                                                                                                                                                                                              hypothetical protein T1N6.10 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52; DB 2;
Pred. No. 3.2;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 1
C;Superfamily: acyl-CoA thiolesterase II
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60.0%;
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llarity 36.8%;
Conservative
4 TYQSRVTHPHLPRALMRSTTK
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Best Local Similarity 60.05
9: Conservative
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142 ELRESRITDPHLPRS 156
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Best Local Similarity
Matches 14; Conserv
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A; Residues: 1-320 <STO>
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cellulose synthase (EC 2.4.1.-) catalytic subunit [validated] - Arabidopsis thaliana collulose synthase (EC 2.4.1.-) catalytic subunit [validated] - Arabidopsis thaliana (C) Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: 20-0ct_2000 #sequence_revision 20-0ct_2000 #text_change 31-Dec-2000
C; Accession: T52054
Science 279, 717-720, 1998
A; Title: Molecular analysis of cellulose biosynthesis in Arabidopsis.
A; Reference number: 213745; MUID: 98111412
A; Ross-references: EMBL: AF027174; PIDN: AAC39336.1
C; Genetics:
A; Note: Ah-B
C; Function: EC 2.4.1.-; cellulose synthase [validated, MUID: 98111412]; involved in as C; Keywords: glycosyltransferase;
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                                                                                                                                                                                                                                                                  C. Accession: B31194
B. Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.
Mol. Cell. B401. B, 3487-3495, 1988
A.Title: The human FGF-5 oncogene encodes a novel protein related to fibroblast growth A; Reference number: A31194; MuID:89096942
A. Accession: B31194
A. Accession: B31194
A. Status: preliminary; not compared with conceptual translation
A. Molecule type: mRNA
A. Residues: 1-38 < ZHA>
A. Cross-references: GB:M23534; GB:M21617; NID:9806636; PIDN:AAB60698.1; PID:9182541
                                                                                                                                                                     hypothetical protein ORFI (FGF 5' region) - human
C;Species: Homo sapiens (man)
C;Date: 12-Jan 1989 #sequence_revision 12-Jan-1989 #text_change 05-Nov-1999
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Pred. No. 1.4;
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   816 CGARPESSVTHPHHHALQPHLPR 838
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69.2%;
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Best Local Similarity 69.2
Matches 9; Conservative
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Gaps

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Indels

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A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: D86215
A;Accession: D86215
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-2254 <STO>
A;Cross-references: GB:AE005172; NID:g8778840; PIDN:AAF79839.1; GSPDB:GN00141
A;Map position: 1
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1985 KTFEEKVSFPHYPKSILKA 2003
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Best Local Similarity 26,38
Matches 5; Conservative
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Search completed: August 26, 2002, 10:04:23 Job time: 69 sec

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August 26, 2002, 10:05:24; Search time 24.08 Seconds (without alignments) 40.199 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                OM protein - protein search, using sw model
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105224 seqs, 38719550 residues 140 1 CGETYQSRVTHPHLPRALMRSTTKC BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-701-623C-5 Title: Perfect score: Scoring table: Sequence: Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	P01854 homo sapien		P06336 mus musculu	Q66220 chinese rap	_	Q60764 mus musculu	_	P24574 halobacteri	P12446 influenza c	æ	S	P11055 homo sapien		P35569 mus musculu	P36078 saccharomyc	rattus	PO4488 herpes simp	human		P04461 oryctolagus			_		P79293 sus scrofa	P02564 rattus norv		~ &		Q9y623 homo sapien	2 homo	3 dictyc	_
SUMMARIES		QI	EPC_HUMAN	EPC_RAT	EPC_MOUSE	RRPO_CRMV	IRS1_RAT	MKR3_MOUSE	GVPC_HALME	GVC1_HALN1	VMAT_INCJJ	MYHD_HUMAN	MYH3_CHICK	MYH3_HUMAN	MYH3_RAT	IRS1_MOUSE	YKI4_YEAST	TRY3_RAT	VGLE_HSV11	Y116_ADE02	HB2D_RAT	MYH7_RABIT	BAR1_HUMAN	RRPO_TVCV	MYH7_MESAU	MYH7_HUMAN	MYH7_PIG	MYH7_RAT	MYH8_HUMAN	MYSS_CHICK	MYH1_HUMAN	MYH4_HUMAN	MYH2_HUMAN	TALA_DICDI	MUC_CANFA
		Length DB	428 1	429 1			1235 1		381 1	382 1	242 1	1938 1	1940 1	1940 1	1940 1	1233 1	116 1	247 1	550 1	106 1	264 1	736 1	1777	1601 1	1934 1	1935 1	1935 1	1935 1	1937 1	1938 1	1939 1	1939 1	1941 1	2492 1	450 1
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		Score	117	80	26	20	49.5	48	47.5	47.5	47	47	47	47	-	46.5	46	46	46	45	45	45	45	45	45				45			45	45	45	44.5
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homo sapien gallus gall caenorhabdi sus scroba homo sapien rattus norv nostoc punc halobacteri homo sapien mesocricetu sorghum bic
P01877 P15979 Q18212 Q29024 Q13838 Q63413 P48971 P33518 Q12968 Q12968 Q43135
ALC2_HUMAN HAIF_CHICK HE47_CAEEL HE47_PIG HE47_PIG OPCA_NOSPU COX1_HALHA NFC3_HUMAN MUC_MESAU CC791_SORBI
340 3455 4254 427 428 428 465 593 1075 454 557
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

ALIGNMENTS

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MEDLINE-83001945; PubMed-6288268; Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.; "Duplication and deletion in the human immunoglobulin epsilon genes."; Cell 29:691-699(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immediate hypersensitivity: modern concepts and developments, pp.1-36, Marcel Dekker, New York (1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [3] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-84236029; PubMed-6234164; MEDLINE-84236029; PubMed-6234164; Flanagan J.G., Rabbitts T.H.; Flanagan J.G., Rabbitts T.H.; "The sequence of a human immunoglobulin epsilon heavy chain constant "The sequence of a human immunoglobulin epsilon heavy chain constant "The sequence of a human immunoglobulin epsilon heavy chain constant "The sequence of a human immunoglobulin epsilon heavy chain constant
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-83186897; PubMed-6300763;
Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,
Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
"Molecular cloning and nucleotide sequencing of human immunoglobulin
epsilon chain cDNA.";
Nucleic Acids Res. 11:719-726(1983).
                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=84207910; PubMed=6327276;
MEDLINE=84207910; Nishida Y., Hisajima H., Honjo T.;
Mishida Y., Hisajima H., Honjo T.;
"Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudogene that lacks introns.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=83065234; PubMed=6815656; Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J Bell L.O., Gould H.J.; "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).
Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
(In) Bach M.K. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A. MEDLINE-83065234; Pubmed-6815656;
                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1GHE.
                   428 AA
                   PRT;
                     STANDARD;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI_TaxID=9606;
                     EPC_HUMAN P01854;
EPC_HUMAN
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'Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-84236092; PubMed-6329728; Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.; Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.; The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison with the human epsilon gene sequence."; EMBO J. 1:1117-1123(1982).
                                                                                                                                                                                                         Hellman L., Pettersson U., Bennich H.; "Characterization and molecular cloning of the mRNA for the heavy (epsilon) chain of rat immunoglobulin E."; Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                            SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
MEDLINE-83182019; PubMed-6820340;
Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
"A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, identification, and DNA sequence.";
DNA 1:335-343(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 429;
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.-> L (IN REF. 2).
D2970B34EF8A72B0 CRC64;
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llarity 60.9%; Pred. No. 6.3e-05;
Conservative 3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Immunoglobulin C region. NoN_TER 1 1 1 CONFLICT 168 168 R \rightarrow N (IN REF. 2) CONFLICT 308 308 P \rightarrow L (IN REF. 2)
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                                 Nucleic Acids Res. 10:6041-6049(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00744; AAA41379.1; ALT_INIT.
                                                                                                                                                                             SEQUENCE OF 205-306 FROM N.A. MEDLINE-82174576; PubMed-6803238;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 4
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Best Local Similarity
Matches 14; Conserv
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REVISIONS.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE-83064537; PubMed-6292865;
Hellman [,., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
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PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 117; DB 1; Length 428; Pred. No. 1.2e-10;
               Padlan E.A., Davies D.R.;
"A model of the F=C= of immunoglobulin E.";
Submitted (JUL-1993) to the PDB data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "FIG=VAR_003885.
25C4CA072AA558A0 CRC64;
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N-LINKED (GLCNAC. .).
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                                                                                                                                                                                                        EMBL; L00022; AAB59424.1; ALT_INIT.
PIR; A02142; EHHU.
PIR; A22771.
PIR; A23195; A23195
PDB; LIGE; 15-JUL-92.
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InterPro; IPR003597; Ig_cl.
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95.7%;
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IGc1; 4.
3D-STRUCTURE MODELING
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Best Local Similarity
Matches 22; Conserv
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SMART; SM00407; IG
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (182 kDa protein) (Contains: Methyltransferase/RNA helicase (MT/HEL) (125 kDa protein)).
Chinese rape mosaic virus (CRMV) (Ollseed rape mosaic virus).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
NCBI_TAXID-42007;
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                                                        SEQUENCE OF 34-421 FROM N.A.
MEDLINE-83117774; PubMed-6818553;
Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
"Cloning and nucleotide sequence of mouse immunoglobulin epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
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Pred. No. 0.31;
3; Mismatches 9; Indels
                   Submitted (APR-1986) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
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CH3.
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EMBL; X01857; CAA25978.1; ---
PIR; A02145; EHMSS.
PIR; A02144; EHMS.
HSSP; P01854; 11GE.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_C1.
InterPro; IPR003507; Ig_C1.
InterPro; IPR003507; Ig_C1.
SMART; SM00410; IG_11ke; 2.
SMART; SM00407; IG_11ke; 2.
SMART; SM00407; IG_11ke; 3.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.0
Best Local Similarity 47.8
Matches 11; Conservative
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415
421 AA;
                                                                                                                                             CDNA.
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Q66220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ć
                                                                                                      "Nucleotide sequence of Chinese rape mosaic virus (oilseed rape mosaic virus), a crucifer tobamovirus infectious on Arabidopsis thaliana.";
                                                                                                                                                                                                                                 -i- FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA CAPPING AND AN RNA HELICASE.
-i- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS BETWEEN CODONS FOR GLW-1103 AND GLN-1105.
                                                                                                                                virus), a crucifer tobamovirus infectious on Arabidopsis thaliana.";
Plant Mol. Biol. 30:191-197(1996).
-!- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
RNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sun X.J., Rothenberg P., Kahn C.R., Backer J.M., Araki E.,
Wilden P.A., Cahill D.A., Goldstein B.J., White M.F.;
"Structure of the insulin receptor substrate IRS-1 defines a unique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding. CHAIN 1 1597 RNA-DIRECTED RNA POLYMERASE. CHAIN 1 1103 METHYLTRANSERASE/RNA HELICASE. NP. BIND 823 8310 ATP (POTENTIAL). VARIANT 919 919 V -> G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                     Aguilar I., Sanchez F., Martin-Martin A., Martinez-Herrera D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50; DB 1; Length 1597; Pred. No. 11;
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35, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STAIN-SPARGUE-DAMLEY; ITSSUE-Liver; MEDLINE-9128784; Pubmed-1648180; Sun X.J., Rothenberg P., Kahn C.R., Backe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U30944; AAB60599.1; -.
InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR002688; V_methyltransf.
InterPro; IPR000606; Viral_helicasel.
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Pfam: PF01443; Viral_helicasel; 1.
Pfam: PF01660; Vmethyltransf; 1.
SEQUENCE FROM N.A.
MEDLINE=96197410; PubMed=8616237;
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MEDLINE=94067102; Pubmed=7504175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA; 181621 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequ
01-NOV-1997 (Rel. 35, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signal transduction protein.", Nature 352:73-77(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.7%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insulin receptor substrate-1.
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Best Local Similarity
Matches 14; Conserv
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919
1286
1597
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us-09-701-623c-5.open.rsp

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
  MKRN3 OR ZFP127 OR ZNF127.
            musculus (Mouse).
                                        NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (
01-JUL-1993 (
15-JUL-1998 (
                                                                                                                                                                                                                                                                                                                                                                Zinc-finger;
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Q02228;
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ZN_FING
ZN_FING
SEQUENCE
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ZN_FING
                                                                                                                           region
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Sun X.J., Crimmins D.L., Myers M.G., Miralpeix M., White M.F.; "Pleiotropic insulin signals are engaged by multisite phosphorylation
                                                                                        Phosphorylation of the insulin receptor substrate IRS-1 by casein kinase II."
J. Biol. Chem. 268:18157-18166(1993).
I Biol. Chem. 268:18157-18166(1993).
FUNCTION: MAY MEDIATE THE CONTROL OF VARIOUS CELLULAR PROCESSES BY INSULIN. WHEN PHOSPHORYLATED BY THE INSULIN RECEPTOR BINDS SPECIFCALLY TO VARIOUS CELLULAR PROTEINS CONTAINING SH2 DOMAINS SIGH AS PHOSPHATIDYLINOSITOL 3.KINASE P85 SUBUNIT OR GRB-2.
SIMILARITY: CONTAINS 1 PTB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                 PHOSPHORYLATION SITES.
MEDLINE-93352637; PubMed-8349691;
Tanasijevic M.J., Myers M.G., Thoma R.S., Crimmins D.L., White M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1235;
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INSR).
INSR).
INSR).
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INSR).
INSR).
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PHOSPHORYLATION (F
PHOSPHORYLATION (F
PHOSPHORYLATION (F
PHOSPHORYLATION (F
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POLY-PRO.
PHOSPHORYLATION (
PHOSPHORYLATION (
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Makorin, 3 (Zinc-finger protein 127)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544 AA
                                                                                                                                                                                                                                                                          EMBL; X58375; CAA41264.1; -.
PIR; S16948; S16948.
HSSP; P35568; IIRS.
InterPro; IPR002404; Insulin_Recep_S-1.
InterPro; IRR010849; PH.
Pfam; PF02174; IRS; 1.
Pfam; PF00169; PH; 1.
                              Cell. Biol. 13:7418-7428(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.4%;
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                                                                                                                                                                                                                                                                                                                                                            SMART; SM00233; PH; 1
SMART; SM00310; PTBI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
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872
1196
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Q60764;
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MOD_RES
MOD_RES
MOD_RES
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MOD_RES
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NCBL_TaxID=2252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Englert C., Krueger K., Offner S., Pfeifer F.;
"Three different but related gene clusters encoding gas vesicles in
                                                  Jong M.T.C., Carey A.H., Caldwell K.A., Lau M.H., Handel M.A., Dissoul D.J., Stewart C.L., Rinchik E.M., Nicholls R.D.; "Imprinting of a RING zinc-finger encoding gene in the mouse chromosome region homologous to the Prader-Willi syndrome genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 1 RING'TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 3 C3H1-TYPE ZINC FINGERS.
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(Rel. 26, Last sequence update)
(Rel. 36, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
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C3H1-TYPE 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:99158; Zfp127.
InterPro; IPR001841; Zf-CCCH.
InterPro; IPR001841; Zf-CCCH.
InterPro; IPR001841; Zf-CCCH.
Pfam; PF00097; Zf-C3H44; 1.
Pfam; PF00642; Zf-CCCH; 3.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                    Mol. Genet. 8:795-803(1999)
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J. Mol. Biol. 227:586-592(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U19106; AAA76863.1; -.
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298
329
401
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Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat
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SEQUENCE FROM N.A.
                      PubMed=10196368;
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Genome Res. 8:1131-1141(1998).

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FUNCTION: MAY CONFER STABILITY TO THE GAS VESICLE MEMBRANES. GAS VESICLES ARE SMALL, HOLLOW, GAS FILLED PROPEIN STRUCTURES THAT ARE FOUND IN SEVERAL PROKAROTIC PLANKTONIC MICROORGANISMS. THEY ALLOW THE POSITIONING OF THE BACTERIA, AT THE FAVORABLE DEPTH FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-RNC.1.1 PLASMID-PURCIOO;
MEDLINE-99063795; PubMed-9847077;
NG W.V., Ciufo S.A., Smith T.M., Bumgarner R.E., Baskin D., Faust J.,
Hall B., Loretz C., Seto J., Slagel J., Hood L., DasSarma S.;
"Snapshot of a large dynamic replicon in a halophilic archaeon:
megaplasmid or minichromosome?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones J.G., Young D.C., Dassarma S.;
"Structure and organization of the gas vesicle gene cluster on the
Halobacterium halobium plasmid pNRC100.";
Gene 102:117-122(1991)
                                                                                      SUBCELLULAR LOCATION: BINDS TO THE EXTERNAL SURFACE OF THE GAS
                                                                                                   VESICLE MEMBRANE.
SIMILARITY: VERY DISTANT, TO GAS VESICLE PROTEINS TYPE C OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 381;
                                                                                                                                                                                                                                                                                                                                                              X APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVC1_HALN1 STANDARD; PRT; 382 AA.
F24514; 09H117;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1992 (Rel. 21, Last sequence update)
03 vesicle protein C l.
03 vesicle protein C l.
04 vector OR GVPC OR VNG5032G) AND (GVPC2 OR VNG5031G).
05 Halobacterium sp. (strain NRC-1), and Halobacterium sp. (strain NRC-10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASP/GLU-RICH (ACIDIC).
9FB48199D0305921 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.9%; Score 47.5; DB 1; 64.3%; Pred. No. 5.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-NRC-1; PLASMID-PNRC100;
MEDLINE-91323716; Pubmed-1864501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42653 MW;
                                                                                                                                                                                                                                                                                                         EMBL; X64701; CAA45944.1; -. PIR; S28115; S28115. Gas vesicle; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-64091, 148370;
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343 CGEYYQA-ITEPHL 355
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59
122
160
192
232
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                                                                                                                                    CYANOBACTERIA.
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Matches 9; Conserv
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Halobacterium
                                                                 GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              halophilic archaea.";
J. Mol. Biol. 227:586-592(1992).
J. Mol. Biol. 227:586-592(1992).
FUNCTION: MAY CONFER STABLLITY TO THE GAS VESICLE MEMBRANES. GAS 'PESICLES ARE SMALL, HOLLOW, GAS FILLED PROTEIN STRUCTURES THAT ARE FOUND IN SEVERAL PROKARYOTIC PLANKTONIC MICROORGANISMS. THEY ALLOW THE POSITIONING OF THE BACTERIA, AT THE FAVORABLE DEPTH FOR
                          SEQUENCE FROM N.A.

STRAIN=NRC-1; PLASMID=PNRC200;
STRAIN=20504483; PubMed=11016950;
MPDLINE-20504483; PubMed=11016950;
MG W.V. Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukia H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Weltl R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.",
"Genome sequence Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-NRC-817; PLASMID=pHH1;
STRAIN-NRC-91021102; PubMed=1404376;
Englert C., Krueger K., Offner S., Pfeifer F.;
"Three different but related gene clusters encoding gas vesicles in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                         STRAIN=NRC-817; PLASMID=PHH1;
MEDLINE=92065812; PubMed=1956294;
Horne M., Englert C., Wimmer C., Pfeifer F.;
"A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis in halophilic archaebacteria.";
Mol. Microbiol. 5:1159-1174(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION; BINDS TO THE EXTERNAL SURFACE OF THE GAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: VERY DISTANT, TO GAS VESICLE PROTEINS TYPE C OF CYANOBACTERIA.
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7 x APPROXIMATE TANDEM REPEATS.
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171DBEB4C0364F46 CRC64;
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7
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Pred. No. 5.8;
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ilarity 64.3%;
Conservative
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42391
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92
130
168
200
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nes 9; Conserv
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Best Local Si
Matches 9
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SEQUENCE
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"The human extraocular muscle myosin heavy chain gene (MYH13) maps to the cluster of fast and developmental myosin genes on chromosome 17."; Genomics 54:188-189(1998).
                                                                                 TISSUE=Extraocular muscle;
MEDLINE=99026150; PubMed=9806854;
Winters L.M., Briggs M.M., Schachat F.;
         OF 1917-1938 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000048; IQ.
InterPro; IPR004009; Myc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   814
1938
186
681
775
130
699
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                                                                                                                                                                                                                                       SUBFRAGMENT (S2)
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Extraocular muscle;
MFISSUE-EXTRAOCULAR muscle;
MFISSOE A., Schiaffino S., Leinwand L.A.;
MFISS A., Schiaffino S., Leinwand L.A.;
MFISS A., Schiaffino S., Leinwand L.A.;
MFISS A., Schiaffino S., Leinwand L.A.;
MFISSOE MISSOE MISSUE MISSOE MISSOE MISSOE
J. MOI., Biol. 290:61-75(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                      MEDLINE-88300888; PubMed-3404579;
Yamashita M., Krystal M., Palese P.;
"Evidence that the matrix protein of influenza C virus is coded for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Q9UXX3; 095252;
L6-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, skeletal muscle, extraocular (MyHC-eo).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 1; Length 242;
Pred. No. 4.3;
                                                                                                                                                                  Influenza C virus (strain C/JJ/50).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 AA; 26967 MW; ABF9D9054E1C9D91 CRC64;
                                                                                                          01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                       242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                       PRT;
                                                                                                                                                                                                                                                                       by a spliced mRNA.";
J. Virol. 62:3348-3355(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.6%;
38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M22038; AAA43781.1; -.
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InterPro; IPR004271; CM1.
Pfam; PF03026; CM1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                       STANDARD;
                     111 11::1 111
344 CGEYYQA-ITEPHL 356
         1 CGETYQSRVTHPHL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                      NCBI_TaxID=11560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matrix protein.
SEQUENCE 242
                                                                                                                                             Matrix protein.
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P12446;
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SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 10 DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 ACTIN-BINDING (BY SIMILARITY).
75 ACTIN-BINDING (BY SIMILARITY).
80 METHYLATION (TRI-) (POTENTIAL).
99 ALKYLATION (SH-1) (POTENTIAL).
09 ALKYLATION (SH-2) (POTENTIAL).
223678 MW; IF6D006416381CD5 CRC64;
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COILED COIL (POTENTIAL).
ATP (POTENTIAL).
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ed. No. 39;
Mismatches 6;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002928; Myosin_tail.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR00169; Myosin_head.
Pfam; PF00736; Myosin_head; 1.
Pfam; PF07736; Myosin_li 1.
Pfam; PF0776; Myosin_tail; 1.
PRINTS; PR00193; MYOSINEAVY.
ProDom; PD000355; Myosin_head; 1.
SMART; SM00105; MY.
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52.9%;
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RSTHPHFVRCLIPNETK 683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. BIOL. Chem. 258:5196-5205(1983).
1. J. BIOL. Chem. 258:5196-5205(1983).
2. I- FUNCTION: MUSCLE MYOSILE SALKALI LIGHT CHAIN SUBUNITS. WISCLE MYOSILE SALKALI LIGHT CHAIN SUBUNITS (MLC).
2. HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC).
3. C. HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC).
3. C. I- SUBCELLULAR LOCATION: Thick filaments of the myofibrils. SHOWING CYCLES OF A 28-RESIDUER REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
3. C. I- PTW. TWO CYSTEINE RESIDUER IN THE S1 DOMAIN ARE SELECTIVELY ALKYLANDONGS: EACH MYOSIN APPASE ACTIVITY.
3. C. I- MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LAFER BE
                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                               Ravinsky C.J., Umeda P.K., Sinha A.M., Elzinga M., Tong S.W., Zak R., Jakvocic S., Rabinowitz M.; Cloned mRNA sequences for two types of embryonic myosin heavy chains from chick skeletal muscle. I. DNA and derived amino acid sequence of
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-87194881; PubMed-3571266;
Molina M.I., Kropp K.E., Gulick J., Robbins J.;
"The sequence of an embryonic myosin heavy chain gene and isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                           01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, fast skeletal muscle, embryonic.
                                                             PRT; 1940 AA
                                                                                                                                                                                                                                                                                                                                               of its corresponding cDNA.";
J. Biol, Chem. 262:6478-6488(1987).
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1502-1940 FROM N.A. MEDLINE-83161144; PubMed-6833296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P08799; IMND.
InterPro; IPR000048; IQ.
InterPro; IPR00409; Wyosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; Myosin_head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                              (Rel. 01, Created)
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                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00015; IQ; 1.
SMART; SM00242; MYSc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00612; IQ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      light meromyosin."
                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                           21-JUL-1986
01-FEB-1996
                                                           MYH3_CHICK
P02565;
                            RESULT 11
                                             MYH3_CHICK
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MYH3_HUWAN STANDARD; PRT; 1940 AA.
P11055; 015492;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, fast skeletal muscle, embryonic (Muscle embryonic myosin heavy chain) (SMHCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of three developmentally controlled isoforms of human
                                                                                                                                                                                                                                                                                                                                                  Gaps
PROSITE; PS50096; IQ; 1. Myosin; Muscle protein; Colled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE-89366648; PubMed-2771643;
Karsch-Mizrachi I., Travis M., Blau H., Leinwand L.A.;
"Expression and DNA sequence analysis of a human embryonic skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-90033298; PubMed-2806546;
Eller M.S., Stedman H.H., Sylvester J.E., Fertels S.H., Wu Q.-L.,
Raychowdhury M.K., Rubinstein N.A., Felly A.M., Sarkar S.;
"Human embryonic myosin heavy chain cDNN. Interspecies sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eller M.S., Stedman H.H., Sylvester J.E., Fertels S.H., Rubinstein N.A., Kelly A.M., Sarkar S.; "Nucleotide sequence of full length human embryonic myosin heavy chain CNNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
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                                                                                                               ATP...
ACTIN BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conservation of the myosin rod, chromosomal locus and isoform specific transcription of the gene."; FEBS Lett. 256:21-28(1989).
                                                                                                                                                                                                                                                                                                               33.6%; Score 47; DB 1; Length 1940; 52.9%; Pred. No. 39;
                                                                                                                                                                                                                                T -> A (IN REF. 2).
ERA -> GRT (IN REF. 2).
W; C34833D75B04DFF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                     IQ.
COILED COIL (POTENTIAL)
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9
                                                                  MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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                                                                                                                                                                                                                  G -> D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89263803; PubMed=2726495;
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Eur. J. Biochem. 189:55-65(1990).
                                                                                                                                                                                                                                                                222816 MW;
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SEQUENCE OF 774-1940 FROM N.A.
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668 RSTHPHFVRCLIPNETK 684
                                                                                                                                                                                                                                                                                                                                                                                 8 RVTHPHLPRALMRSTTK 24
                                                                                                                                                                                                                                                                                                                                                 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain cDNA.
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                                                                                                                                                                                                                                 CONFLICT
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                                                                                                 DOMAIN
NP_BIND
DOMAIN
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MOD_RES
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                    VARIANT
                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
MYH3_HUMAN
                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                  -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILES.
-1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN APPASE ACTIVITY.
-1- MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
A -> G (IN REF. 3).
K -> OE (IN REF. 1 AND 2).
SR -> RA (IN REF. 1).
SR -> CT (IN REF. 2).
RG -> OT (IN REF. 2).
                                                                                                                                                                                                                                            SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myosin; Muscle protein; Coiled coil; Thick filament; Acti
Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43CA58C6A4BA1253 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQ.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL).
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR004009; Myosin_Lail.
InterPro; IPR001509; Myosin_tail.
InterPro; IPR001509; Myosin_head.
Pfam; PF00612; IQ; 2.
Pfam; PF0063; Myosin_head; 1.
Pfam; PF001576; Myosin_Lail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; Myosin_head; 1.
SMART; SM00015; IQ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, X13988; CAA32167.1; --
EMBL, X1100; CAA31492.1; --
EMBL, X15593; CAA35942.1; --
EMBL, X15696; CAA33731.1; --
EMSL, X04090; S04090.
HSSP; P08799; IMMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50096; IQ; 1.
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811
1933
186
678
772
130
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706
1331
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1608
1663
1940
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NP_BIND
DOMAIN
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Mismatches

Conservative

Query Match Best Local Similarity Matches 8, Conserv

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RATE AND ADDRESS OF A LIGHT CHAIN SUBDILIER.

REAL TOOMPLEE INCLEDECTION GENE. EVIDENCE against intron-dependent evolution for the roof.";

TO MOI. Biol. 190:291-317(1986).

1. FUNCTION: MUSCLE CONTRACTION.

1. SUBDILIT MUSCLE MOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBDILITS (MHC), 2 ALKALL LIGHT CHAIN SUBDILITS (MHC).

2. FEGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

2. SUBDILIT MUSCLE COATION. THICK filaments of the myofibrils.

2. FEGULATORY LIGHT CHAIN SUBUNITS (MLC).

3. MND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC).

4. FUNCTION: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES.

3. CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

4. CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

5. CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

5. CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

6. IP PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

5. MISCLELANBOUS: EACH MYOSIN HEWY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (HMM). IT CAN LAFER BE COLLED TO THE COLLS.

5. SPLIT FIRTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myosin; Muscle protein; Colled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation; Multigene family.

Multigene family.

MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-87060988; PubMed-3783701;
Strehler E.E., Strehler-Page M.-A., Perriard J.C., Perlasamy M.,
Nadal-Ginard B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBFRAGMENT (S2).
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                01-OCT-1989 (Rel. 12, Created)
1-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 10, Last annotation update)
Myosin heavy chain, fast skeletal muscle, embryonic.
                                                                                                                                                       PRT; 1940 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P08725, A24321, HSSP; P1R; A24922, HSSP; P08799; IMND.
InterPro; IPR000049; Myosin_N: InterPro; IPR000049; Myosin_tail.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR002917; Spectrin.
InterPro; IPR002017; Spectrin.
InterPro; IPR001609; Myosin_head.
Pfam; PF000612; IQ; 2.
Pfam; PF00063; Myosin_head; 1.
Pfam; PF00193; Myosin_tail; I.
PRINTS; PR00193; MYOSINHEAVY.
PR000m; PD000355; Myosin_head; 1.
SWART; SM00015; IQ; 1.
PROSITE; PS50096; IQ; 1.
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664 RTTHPHFVRCIIPNETK 680
8 RVTHPHLPRALMRSTTK 24
                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                       MYH3_RAT
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us-09-701-623c-5.open.rsp

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YKL084W
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                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1172:323-326(1993).

-!- FUNCTION: MAY MEDIATE THE CONTROL OF VARIOUS CELLULAR PROCESSES
BY INSULIN. WHEN PHOSPHORYLATED BY THE INSULIN RECEPTOR BINDS
SPECIFICALLY TO VARIOUS CELLULAR PROTEINS CONTAINING SH2 DOMAINS
SUCH AS PHOSPHATIDYLINOSITOL 3-KINASE P85 SUBUNIT OR GRB-2.
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
-!- SIMILARITY: CONTAINS 1 PTB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                   Araki E., Haag B.L. III, Kahn C.R.; "Cloning of the mouse insulin receptor substrate-1 (IRS-1) gene and
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93192326; PubMed-8448209;
Keller S.R., Aebersold R., Garner C.W., Lienhard G.E.;
"The insulin-elicited 160 kpa phosphotyrosine protein in mouse
adipocytes is an insulin receptor substrate 1: identification by
                                                                                                                                                ;
0
                      ATP (POTENTIAL).
ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
ALKYLATION (SH-2).
                                                                                                                         DB 1; Length 1940; 39;
                                                                                                                                                Indels
    IQ.
COILED COIL (POTENTIAL)
                                                                                                                                                9
                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                 PRT; 1233 AA
                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         complete sequence of mouse IRS-1.";
Biochim. Biophys. Acta 1221:353-356(1994).
                                                                                                                          Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002404; Insulin_Recep_S-1.
InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94220494; PubMed=8167159;
                                                                                                                                                                                                                                                                     (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                     Insulin receptor substrate-1.
IRS1 OR IRS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L24563; AAA39335.1; -. EMBL; X69722; CAA49378.1; -.
                                                                                                                         33.68;
47.18;
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664 RTTHPHFVRCIIPNETK 680
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                                                                                                                                                Conservative
                                                                                                                                                                                                                                               STANDARD;
                         186
678
772
130
696
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Pfam; PF00169; PH; 1.
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MGD; MGI:99454; Irsl.
                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
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                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                    01-JUN-1994
                                                                                                                                                                                                                                              IRS1_MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1233;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Hypothetical 13.6 kDa protein in MDH1-VMA5 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
PHOSPHORYLATION (BY INSR)
(BY SIMILARITY).
PHOSPHORYLATION (BY INSR)
(BY SIMILARITY).
PHOSPHORYLATION (BY INSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Pohl T.M., Pohl F.M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H -> R (IN REF. 2).

IN; C0E9B2D890DADD87 CRC64;
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$0001567; XKL084W.
thetical protein.
ENCE 116 AA: 13641 MW; 57464E5FD9A591F8 CRC64;
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PHOSPHORYLATION (BY INSR)
                                                                                                                                                                                                                                      PHOSPHORYLATION (BY INSR)
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PHOSPHORYLATION (BY INSR)
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MISSING (IN REF. 2).
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PHOSPHORYLATION (BY
                                                                                                                                                                                                                  (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.2%; Score 46.5; [43.5%; Pred. No. 29; iive 2; Mismatches
                                                                                                                   POLY-SER.
POLY-GLN.
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                                        PH_DOMAIN; 1.
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SMART; SM00233; PH; 1.
SMART; SM00310; PTBI; 1.
PROSITE; PS50003; PH_DOW
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Best Local Similarity
Matches 10; Conserv
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DOMAIN 12
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SEQUENCE 11
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P36078;
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      Query Match
      32.9%; Score 46; DB 1; Length 116;

      Best Local Similarity 45.0%; Pred. No. 2.8;

      Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

      Qy 6 QSRVTHPHLPRALMRSTTKC 25

      11 | 11: :: 11

      Db 14 QSRCVHWHLPRDVIAIRFKC 33

      Search completed: August 26, 2002, 10:17:02

      Job time: 698 sec
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091002 arabidopsis

089465 influenza c

067390 influenza c

0904031 influenza c

091457 influenza c

091457 influenza c

091457 influenza c

0998812 influenza c

099882 influenza c

0998851 influenza c

099885 influenza c

090405 influenza c

067388 influenza c

067381 influenza c

067381 influenza c

067392 influenza c

067392 influenza c

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R Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney B.C.,
R Flajnik M.F.;
"A new antigen receptor gene family that undergoes rearrangement and
extensive somatic diversification in sharks.";
IL Nature 374.168-173(1995)
IL Mature 374.168-173(1995)
IL Mature 374.168-173(1995)
IR HSSP; P01709; 2McG.
R InterPro; IPR003509; Ig_Alike.
R InterPro; IPR003509; Ig_Alike.
R InterPro; IRR003006; Ig_Alike.
R InterPro; ICG:1, A. SMO0407; IGC:1, A. SMART; SMO0401; IGC:1, R. SMART; SMO04010; IGC:1, R. SMART; SMO04010; IGL:1, R. SMART; SMO04010; IG_Alike; 2.
RR POSTITE: PS00229: IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                            Ginglymostoma cirratum (Nurse shark).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes; Ginglymostomatidae; Ginglymostomatidae; Ginglymostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
NOVEL ANTIGEN RECEPTOR.
2FF9D2071CDA6DFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NOVEL ANTIGEN RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
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Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                      684 AA
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                                                                                                      09W841
09W8X9
09WAD5
09WAD7
09WAD7
09WAE2
09WAE2
09WAE2
067388
067391
067391
067392
0918N4
                 Q9EN02
Q89465
Q67390
Q9WAD3
Q9UQ57
Q91Q55
Q39842
Q95SH2
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57.1%;
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Best Local Similarity
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TISSUE=SPLEEN;
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684
                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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090544
O9sys4 sambucus ni
O9sys5 sambucus ni
O9sys5 sambucus ni
O9rjy0 streptomyce
O9rio sambucus ni
O9lpa7 ribgrass mo
O88603 tobacco mos
O9lpa8 ribgrass mo
O88604 tobacco mos
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09vfl6 drosophila
09ltK6 arabidopsis
09v9x5 drosophila
0918n3 rana pipien
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                                                             August 26, 2002, 10:04:29; Search time 66.82 Seconds (without alignments) 64.724 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                             562222
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                           hits satisfying chosen parameters:
                                                                                                                                                                          562222 seqs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries
                                              protein search, using sw model
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095854
095855
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091PA7
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Q9I8N3
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_manmal:*
sp_mhc:*
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sp_phage:*
sp_plant:*
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3377.2
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Score

Result Š. Total number of

Searched:

Minimum DB : Maximum DB :

Database :

Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

3

Gaps

15;

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A Van Danne E.J.M., Charals D., Roy S., Tierens K., Barre A.,

MEDLINE-99214486; PubMed=10198114;

MEDLINE-99214486; PubMed=10198114;

A Van Danne E.J.M., Charals D., Roy S., Tierens K., Barre A.,

Martins J.C., Rouge P., Van Leuven F., Does M., Peumans W.J.;

Thomologous to PR-4 and class V chitinase genes.";

L plant Physiol. 119:147-1556(1999).

R EMBL; AF074388; AAD12237.1;

R HSSP; PO2877; IHEV.

R InterPro: IPRO1002; Chitin_bind.

R InterPro: IPRO00726; Glyco_hydro_19,

Pfam; PF00187; chitin_binding; 1.

R Pfam; PF00187; chitin_binding; 1.

R Pfam; PF00187; CHITINBINDNG.

R PRINTS; PRO0451; CHITINBINDNG.

R PRODOM: PD000674; Glyco_hydro_19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HEVEIN-LIKE PROTEIN HIPF (FRAGMENT).
Sambucus nigra (European elder).
Sumbucus, viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                              Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 333;
homologous to PR-4 and class V chitinase genes.";
Plant Physiol. 119:1547-1556(1999).
REMEL, AF074387, AA011408.1; -.
HSSP: P02877; 11EV.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR0010726; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
ProDom; P001082; Glyco_hydro_19; 1.
ProDom; P0000574; Glyco_hydro_19; 1.
ProDom; P0000609; Chitin_bind; 1.
SMART; SM00270; Chtell; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
Chitin-binding: 333 AA; 37126 MW; 3231BD42F4352CE5 CRC64;
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37047 MW; 3913256EBC3577B9 CRC64;
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Pred. No. 1.8;
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                                                                                                                                                                                                                                                                                Query Match 38.2%; Score 53.5; D
Best Local Similarity 42.9%; Pred. No. 1.8;
Matches 15; Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
Matches 15; Conserv
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida II; Adoxaceae; Sambucus.

NCBI_TaxID-4202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sambucus nigra (European elder).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eussterida II; Adoxaceae; Sambucus.

NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

TISSUE-ELDERBERRY FRUIT;

WEDLINE-9211486; Pubmed-10198114;

Van Damme E.J.M., Charels D., Roy S., Tierens K., Barre A.,

Martins J.C., Rouge P., Van Leuven F., Does M., Penmans W.J.;

"A gene encoding a hevein-like protein from elderberry fruits is phomologous to PR-4 and class V chitinase genes.";

Plant Physiol. 119:1547-1556(1999).

EMBL; AF074385; AAD11406.1;

HSSP; P02877; IHEV.
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TISSUE-ELDERBERRY FRUIT;
MEDLINE-99214486; Pubmed-10198114;
Van Damme E.J.M., Charels D., Roy S., Tierens K., Barre A.,
Martins J.C., Rouge P., Van Leuven F., Does M., Peumans W.J.;
"A gene Ancoding a hevein-like protein from elderberry fruits is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
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        Indels
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                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HEVEIN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09SYS4,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HEVEIN-LIKE PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR0012; chitin_binding; 1.
Pfam; PF00182; chitin_binding; 1.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000574; Glyco_hydro_19; 1.
PROSITE; PS00774; CHITIN_BINDING; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
                                                                                                                                                   PRT;
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                                      4 TYQSRVTHPHLPRALMRSTTK
      Conservative
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Best Local Similarity
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      12;
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Q92T61;
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Chitin-binding
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01-DEC-2001
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                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                              STRAIN—CV. COLUMBIA;
Liu S., Chan A., Yu G., Lee J., Lenz C., Pham P., Sakano H.,
Liu S., Chan A., Yu G., Lee J., Lenz C., Pham P., Sakano H.,
Toriumi M., Chin C., Chiou J., Choi E., Chung M., Gonzalez A.,
Howng B., Liu A., Vaysberg M., Altafi H., Brooks S., Buehler E.,
Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C., Khan S.,
Kim C., Lam B., Miranda M., Nguyen M., Palm C., Shinn P.,
Southwick A., Davis R., Ecker J., Federspiel N., Theologis A.;
"The sequence of BAC TlN6 from Arabidopsis thaliana chromosome 1.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
HSSP; P23911; 1C8U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                         InterPro; IPR003703; Acyl_CoA_thio.
Pfam; PF02551; Acyl_CoA_thio; 1.
SEQUENCE 320 AA; 36157 MW; 03A82A96333E1BFC CRC64;
                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
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                                 320
                                                        Created)
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MEDLINE-97000351; PubMed-8843436;
                                                    01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                              PRELIMINARY;
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142 ELRESRITDPHLPRS 156
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Best Local Similarity
Matches 9; Conserv
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SEQUENCE FROM N.A.
STRAIN=A3(2);
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SEQUENCE FROM N.A.
                                                                                                                                                           NCBI_TaxID=3702;
                                                                                        TIN6.10 PROTEIN
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Mol. Microbiol. 21:77-96(1996).
--- SOBCELLUAR LOCATION: INTEGRAL MEMBRANE PROFEIN (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
EMBL, AL133210; CAB61602.1; --
INTERPRO; PRR003662; sub_transporter.
InterPro; IPR003662; sub_transporter.
PINTERPOS INTERPROPERTY: 1.
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MEDLINE=99214486; PubMed=10198114;
MEDLINE=99214486; PubMed=10198114;
MacDLINE=99214486; PubMed=10198114;
MacDLINE=99214486; PubMed=1018114;
MacDline E.V., Rouge P., Van Leuven F., Does M., Peumans W.J.;
MacGline Encoding a hevein-like protein from elderberry fruits homologous to PR-4 and class V chitinase genes.";
Plant Physiol. 119:1547-1556(1999).
EMBL; AF074386; AAD11407.1;
HSSP; P02877; 1HEV.
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Last sequence update)
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Pred. No. 5.
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Pred. No.
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InterPro; IPR000726; Glyco_hydro_19.
Pfam: PF00187; chitin_binding; 1.
Probom: PP00182; Glyco_hydro_19; 1.
Probom: PD000574; Glyco_hydro_19; 1.
Probom: PD000609; Chitin_bind; 1.
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PROSITE; PS00774; CHITINASE_19_2;
PROSITE; PS00026; CHITIN_BINDING;
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                                                                                                                                                                                                         533 AA; 54474 MW;
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58.8%;
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                                                                                                                                    Pfam; PF00083; sugar_tr;
PRINTS; PR01036; TCRTETB.
Transmembrane.
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Best Local Similarity 40.0
Matches 14; Conservative
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Matches 10; Conserv
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Length 1107; Indels

12;

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Dorokhov Y.L., Ivanov P.A., Novikov V.K., Yefimov V.A., Atabekov I.G., "Tobamovirus of cruciferous plants: nucleotide sequence of genes of the transport protein, capsid protein, and 3'-terminal untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SHANGHAI;
MEDLINE-21395181; PubMed-11504428;
Zhu H., Hong J., Ya R., Chen J., Yu S., Adams M.J.;
Sequence analysis shows that Ribgrass mosaic virus Shanghai isolate (RMV-Sh) is closely related to Youcal mosaic virus.";
Arch. Virol. 146:1231-1238(2001).
                                                                                                                                                                                                                                                                                                                                                                                 Virúses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
NCBI_TaxID=51680;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
NCBI_FaxID=12242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhu H., Hong J., Chen J., Yu S.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF514924; AAK53541.1;
SEQUENCE 1597 AA: 181462 MW; 9E6576FF595E0DEF CRC64;
                                               D6727409DB51A651 CRC64;
                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) RNA REPLICASE READ-THROUGH COMPONENT.
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Last annotation update)
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36.8%; Pred. No. 34;
iive 4; Mismatches 6
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23;
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                                                                                            Score 50;
Pred. No. 2
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 InterPro; IPR002588; V_methyltransf.
Pfam; PF0148; Viral_nellossel; 1.
Pfam; PF01660; Vmethyltransf. 5.
SEQUENCE 1107 AA; 125177 WW; D67
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MEDLINE~94341372; Pubmed-7545946;
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36.8%;
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01,
19,
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                                                                                             Query Match 35.7
Best Local Similarity 36.8
Matches 14; Conservative
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nes 14; Conservative
                                                                                                                                                                                                                                                                          PRELIMINARY;
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01-DEC-2001 (
01-DEC-2001 (
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Q91PA8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dorokhov Y.L., Ivanov P.A., Novikov V.K., Yefimov V.A., Atabekov I.G., "Tobamovirus of cruciferous plants: nucleotide sequence of genes of the transport protein, capsid protein, and 3'-terminal untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete nucleoide sequence and genome organization of a tobamovirus infecting cruciferae plants."; FEBS Lett. 350:5-8(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dorokhov Y.L., Ivanov P.A., Novikov V.K., Efimov V.A., Atabekov I.G., Efimov Y.A., Casper R., Atabekov J.G., 'obamovirus of the Cruciferae family: nucleotide sequence of the 5'-untranslated region and nonstructural protein genes controlling
                                                                                                                                          Zhu H., Hong J., Ye R., Chen J., Yu S., Adams M.J.;
"Sequence analysis shows that Ribgrass mosaic virus Shanghai isolate (RMV-Sh) is closely related to Youcai mosaic virus.";
Arch. Virol. 146:1231-1238(2001).
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                     Ribgrass mosaic virus (RMV).
Viruses: ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
NCBI_TaxID=51680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tobacco mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Belenovich E., Generozov E., Novikov V., Zavriev S.; "Properties and the genome structure of the K2 strain of tobacco
                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 1103; 23;
                                                                                                                                                                                                                                      STRAIN-SHANGHAI;
Zhu H., Hong J., Chen J., Yu S.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF244924; AAK53540.1; -
SEQUENCE 1103 AA; 124750 WW; FD9BD83F500C70FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    1031 GETYEKTAIVRLTATPLEIISRASPHVLVALTRHTTRC 1068
                                                                                                                                                                                                                                                                                                                                                                                                                2 GETYQS----RVT------HPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1107 AA
                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replication viral genome.";
Dokl. Akad. Nauk SSSR 335:792-798(1994).
                                                                                                                                                                                                                                                                                                                                                    Score 50;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dokl. Akad. Nauk SSSR 332:518-522(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mogaic virus.";
Mol. Biol. (Mosk.) 0:0-0(0).
Embl. 229370; CA882558.1; -.
InterPro. IPR000606; Viral_helicasel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                           MEDLINE-21395181; PubMed-11504428;
                                                                                                                                                                                                                                                                                                                                                    35.7%;
36.8%;
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                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 36.8
Matches 14; Conservative
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                  RNA REPLICASE COMPONENT
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SEQUENCE FROM N.A.
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                                                                                                            STRAIN-SHANGHAI;
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14;

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273 AA

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PRELIMINARY;
                                                                             CG9612 PROTEIN.
                                            01-MAY-2000
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01-DEC-2001
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                        Q9VFL6
                                   Q9VFL6
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 Dorokhov Y.L., Ivanov P.A., Novikov V.K., Agranovsky A.A., Morozov S.,
Efimov V.A., Casper R., Atabekov J.G.;
                       Complete nucleotide sequence and genome organization of a tobamovirus
                                                                         Dorokhov Y.L., Ivanov P.A., Novikov V.K., Efimov V.A., Atabekov I.G., Efimov V.A., Casper R., Atabekov J.G.; "obamovirus of the Cruciferae family: nucleotide sequence of the 5'-untranslated region and nonstructural protein genes controlling pokl. Akad. Nauk SSSR 335:792-798(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Adoxaceae; Sambucus.
                                                                                                                                                                 Belenovich E., Generozov E., Novikov V., Zavriev S.; "Properties and the genome structure of the K2 strain of tobacco
                                                                                                                                                                                                                                                                                                                                                                 14;
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                                                                                                                                                                                   mosaic virus.";

Robert Mosk.) 0:0-0(0).

R EMBL; 229370; CAA8559.1; -.

R InterPro: IPR001788; RNA.dep.RNApol2.

R InterPro: IPR001788; RNA.dep.RNApol2.

R InterPro: IPR002588; V.methyltransf.

R InterPro: IPR002588; V.methyltransf.

R Ffam; PF00978; RNA.dep.RNApol2; 1.

DR Pfam; PF00443; Viral.helicasel; 1.

DR Pfam; PF00466; Viral.helicasel; 1.

DR Pfam; PF00466; Vmethyltransf; 1.

DR Pfam; PF00466; Vmethyltransf; 1.

DR Pfam; PF00466; Vmethyltransf; 1.

DR PR05ITE; PS00118; EF_HAND: UNKNOWN.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Hevein-like proteins from Sambucus nigra leaves.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF434174; AAL30421.1; -
SEQUENCE 330 AA: 36732 MW; 8FCDDA8576B110DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49.5; DB 10;
Pred. No. 7.6;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 12;
Pred. No. 34;
4; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 AA
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                                infecting cruciferae plants.";
FEBS Lett. 350:5-8(1994).
                                                                                                                                                                                                                                                                                                                                           35.7%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 19, C
(TrEMBLrel. 19, I
(TrEMBLrel. 19, I
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Best Local Similarity 36.8
Matches 14; Conservative
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                                                               SEQUENCE FROM N.A.
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01-DEC-2001
01-DEC-2001
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Q944B9
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RK STRAIN-ERKENEEN;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides F.G., Scherer S.E., Il P.W., Evans C.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andraws-Pfannkoch C., Bladwin D.,
RA Ballew R.M., Basun M.R., Bandari D., Bolshakov S.,
Berkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
RA Berkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., B. Davies P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., B. Davies P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Brottier P.,
RA Burtis K.J., Doup L.E.,
Downes M., Dugan R.C., Garrilla H., Gu Z., Guan P.,
RA Burtis N.J., Harvay D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvay D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hull M. Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
Alut X., Mattei B., McIntosh T.C., Muzny D.M., Nelson D.L.,
Ra Merkulov G., Milshina N.V., Mobarry C., Morris S., Way M.S.,
Rainert K., Remington K.A., Howland T., Strong K., Wasserman D.A.,
Reinert K., Remington K.A., Worley K.C., Wu D., Yang X.,
Nang Z.-Y., Wassarman D.A., Weinstock M., Walssenbed J.,
Walliams S.M., Woodage T., Simpson M., Strong K., Wang K., Simth H.,
Rainer K., Bong S.P., Lens K., Worley K.C., Wu D., Yang S., Zhan K.,
Rainer K., Brong P.W., Rolley K., Wu D., Wulley R.,
Rainer K., Brong S., Rainer
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                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha,
Ephydroidea; Drosophilidae, Drosophila.
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(TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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Pred. No. 7.5;
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53.3%;
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FlyBase; FBgn0038216; CG6
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Q9LTK6
ID Q9LTK6
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Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celliker S.E., Holf R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.E., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Boyle C., Batzer B.G., Helf G., Nelson C.R., Miklos G.L.G.,
An Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Bortova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Bortova D., Botchan M.R., Doug Z., Mays A.D., Dew I., Dietz S.M.,
A charly J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A charly S., Doup L.E., Downes M., Dugan-Rocha S., Duukov B.C., Dunn P.,
Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Duukov B.C., Dunn P.,
A dolodek A., Gong F., Gerraz C., Ferriar S., Fleischman W.,
Rosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
A Jalali M., Kalush F., Karpen G. H., Re Z., Kennison J.A., Ketchum K.A.,
A Jalali M., Kalush F., Karpen G. H., Re Z., Kennison J.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A Liu X., Mattel B., Morlitosh T.C., Moreled M.P., Morberson D.,
A Mortulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
A Moutt S.M., Mourphy B., Murphy L., Muzny D.M., Nelson D.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae: Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                             Kaneko T., Katch T., Asamizu E., Sato S., Nakamura Y., Kotani H., Tabata S.,
                                                                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AB025603; BAA97457.1; - SEQUENCE 277 AA; 31592 MW; C72F0D844D6A2089 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
GENOMIC DNA, CHROMOSOME 5, BAC CLONE:F17P19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 AA.
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MEDLINE=20196006; Pubmed=10731132;
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Matches 8; Conserv
                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                NCBI_TaxID=3702;
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Q9V9X5
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Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A. H., Wang X., Wang S.Y., Wassarman D.A., Weinstock G.W., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Mul D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Mink M., Csiszar K.; The role of Drosophila lysyl oxidase in the regulation of chromatin "The role of Drosophila
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10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  structure.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003779; AARF51153.1;
EMBL; AJ295625; CAB99480.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001695; Lysyi_oxidase.
InterPro; IPR001199; SRCR.
Pfam; PF01186; Lysyl_oxidase; 1.
Pfam; PF01316; Lysyl_oxidase; 1.
PRINTS; PR00074; LYSYLOXIDASE.
PRINTS; PR000758; SPERATTRCPTR.
ProDom; PD013887; Lysyl_oxidase; 1.
SMART; SM00202; SR; 1.
SROSTTE; PS02087; SRCR. 2; 1.
SEQUENCE 360 AA; 40832 MW; 7130F7265CB5B698 CRC64;
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Best Local Similarity 40.9
Matches 9; Conservative
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Search completed: August 26, 2002, 10:16:17 Job time: 708 sec

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Sequence 4
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US-09-049-577-4
US-09-390-598-4
US-09-390-598-4
US-08-564-972-34
US-08-786-748A-53
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US-08-932-682-67
US-09-152-934-12
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US-09-153-396A-218
US-09-153-396A-218
US-09-488-799-45
US-09-488-799-45
US-09-488-799-45
US-08-686-599A-11
US-08-986-598A-11
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Pred. No. 8e-09;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPEREATING SYSTEM: PC WILLUCTURENT PAPELLATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTONNEY,AGENT INFORMATION:
NAME: MARIE H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
FELECHONE: 212-758-4800
TELEPHONE: 212-751-6849
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TELEGHORE: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-100-414B-95; Sequence 95, Application US/09100414B; Patent No. 6025468; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
CONTACT OF WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.6%;
64.0%;
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Matches 16; Conservative
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MOLECULE TYPE: peptide
    CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan &
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Query Match
  RESULT
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Sequence 19, Appl.
Sequence 10, Appl.
Sequence 5, Appl.
Sequence 5, Appl.
Sequence 23, Appl.
Sequence 24, Appl.
Sequence 23, Appl.
Sequence 37, Appl.
                                                                                                                                           August 26, 2002, 10:19:37; Search time 33.13 Seconds (without alignments) 18.432 Million cell updates/sec
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Sequence 9, 1
Patent No. 51
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Sequence 9,
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/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_AA:*
                                                                                                                                                                                                                                         US-09-701-623C-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                              Searched:
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Result No.

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Gaps
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Pred. No. 0.005;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MCDIUM TYPE: 35 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: 1gE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                         P0718P3
                                                     FILING DATE: 21-Apr.1994
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION NUMBER: 08/174768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION: NAME: SVODGA, CRAIG G. REGISTRATION NUMBER: 39,044
REFERENCE/COCKET NUMBER: 90,1893
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/08232539D Patent No. 5965709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GETYKSTVSHPDLPREVV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | | : | : | | | | : | : | 5 | GETYQCRVTHPHLPRALM 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.69
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
SOFTWARE: WinPati
                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: Linear
US-08-232-539D-19
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-232-539D-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READBLE FORM:
NEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-noc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                 Sequence 95, Application US/09303323
| Patent No. 6228987
| GENERAL INFORMATION:
| APPLICANT: Wang, Chang Yi
| TITLE OF INVENTION: IMMUNOGENS
| TITLE OF INVENTION: IMMUNOGENS
| CORRESPONDENCES: 106
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Morgan & Finnegan, L.L.P.
| STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-232-5390-19
Sequence 19, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: IgE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                 CONDITY: USA
CONDITY: USA
DIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION NUMBER: 09/100,414
FILING DATE: 20-UNME-1998
ATTERNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREE: Genentech, Inc.
STREE: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 69.6%;
Best Local Similarity 64.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-09-303-323-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
SULT 2
-09-303-323-95
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US-09-077-991-5
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                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Alnemri, Teresa
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140 434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT APPLICATION NUMBER: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 22
                                                                                                                                                                                        Gaps
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DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
86
                                                                                                                                               Score 58; DB 2; Length 24;
Pred. No. 0.0055;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 4; Length 22; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09017205
Fatent No. 5965357;
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DEPTIDE STRUCTURES AND THEIR USE ITILE OF INVENTION: DIGGNOSIS OF HERPES SIMPLEX VIRUS:
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon & Vanderhye PC
STREET: Alington
STREET: Wirginia
CITY: Alington
STREET: Virginia
COUWTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin NoTA:
APPLICATION NUMBER: US/09/017,205
FILING DATE: 02-FEB-1998
CLASSIFICATION: 435
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                                                                                                                                                 43.0%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                        2 GETYKSTVSHPDLPREVV 19
                                                                                                                                                                                                                                           7 GETYQCRVTHPHLPRALM 24
                                                                                                                                               Query Match
Best Local Similarity 55.6%
Matches 10; Conservative
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 42.9
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Mus musculus
US-09-187-789-10
                                                     TYPE: Amino Acid
TOPOLOGY: Linear
                                                                     ; TOPOLOGY:
US-08-232-539D-20
                                                                                                                                                                                                                                                                                                                              -09-187-789-10
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US-09-017-205-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Subramaniam, M.
APPLICANT: Spelsbergy T.C.
APPLICANT: Spelsbergy T.C.
APPLICANT: Spelsbergy T.C.
APPLICANT: Spelsbergy T.C.
TITLE OF INVENTION: TGF-Beta inducible early factor-1
TITLE OF INVENTION: (TIEF-1) and a method to detect breast cancer: FILE REFERENCE: 150.157025
CURRENT APPLICATION NUMBER: US/09/077,991
CURRENT FILING DATE: 1996-07-07
EARLIER APPLICATION NUMBER: PCT/US96/19555
EARLIER PILING DATE: 1996-12-11
EARLIER PILING DATE: 1995-12-11
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                        Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Chad, Nir
APPLICANT: Kadegari, Ramin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: The Regents of the University of California
                                                                                                                                                                                                                                 peptide from HSV-2 glycoprotein G internal
                                                                                                                                                                                                                                                                                                                                   Score 35; DB 2;
Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 4
Pred. No. 26;
1; Mismatches
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-436
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 298, Application US/09177249
Patent No. 6229064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 5, Application US/09077991
; Patent No. 6207375
                                                                                                      TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.9%;
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                        Query Match 25.9
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ETYKSTVSHPDLPR 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-077-991-5
                                                                                                                                                                                                                  linear
                                                                                                                                                                                                           ; TOPOLOGY: line; MOLECULE TYPE: E; FRAGMENT TYPE: i
                                                                                                                                                                                                                                                                                                                                                                                                                         13 DLPREVVR 20
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                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Ian M. Whitehead
APPLICANT: Ian M. Whitehead
APPLICANT: Alan Slusarenko
APPLICANT: Alan Brash
APPLICANT: Alan Brash
APPLICANT: Nathalie Tijet
TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
TITLE OF INVENTION: LYASE AND USES THEREOF
FILE REFERENCE: 06027.0001
CURRENT APPLICANTION NUMBER: US/09/078,173A
CURRENT APLICATION NUMBER: 1998-05-13
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FRSESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ian M. Whitehead
APPLICANT: Alan Slusarenko
APPLICANT: Duncan Gaskins
APPLICANT: Duncan Gaskins
APPLICANT: Alan Brash
APPLICANT: Nathalie Tijet
TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
TITLE OF INVENTION: AVASE AND USES THEREOF
FILE REFERENCE: 06027.0001
CURRENT APPLICATION NUMBER: US/09/078,173A
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 24
LENGTH: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 13;
65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-078-173A-24
Sequence 24, Application US/09078173A
Patent No. 6200794
                                                                                                                                                                                                                          Sequence 23, Application US/09078173A Patent No. 6200794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Psidium Guajava (guava)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Psidium Guajava (guava)
US-09-078-173A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.0%;
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Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 23.0
Best Local Similarity 46.2
Matches 6; Conservative
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               5 YKSTVSHPDLP 15
                                                 GENERAL INFORMATION:
                                                                                                                                                               RESULT 10
US-09-078-173A-23
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US-07-976-358-24
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LENGTH: 13
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0
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit TITLE OF INVENTION: Development in Plants
FILE REFERENCE: 023070-08612005
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 298
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 4; Length 18; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.0%; Score 31; DB 1; Length 11; 45.5%; Pred. No. 53; 4; Indels ive 2; Mismatches 4; Indels
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2 IP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: Date of the property of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rearden, Ann
TITLE OF INVENTION: A NOVEL AUTOANTIGEN, PINCH
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-269441A-15
Sequence 15, Application US/08269441A
Patent No. 5552529
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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LENGTH: 11 amino acids
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Best Yocal Similarity 45.5
Matches 5; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Arabidopsis sp. US-09-177-249-298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
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; LOCATION: 1..11
US-08-269-441A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 REVVRSIAKC 25
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us-09-701-623c-84.closed.rai

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APPLICANT: FIELDS, Howard A.
APPLICANT: FIELDS, Howard A.
APPLICANT: FIELDS, Howard A.
APPLICANT: FAVOROV, Yuri
APPLICANT: FAVOROV, Wichael
TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1.4e+02;
1; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/976,358
FILING DATE: 19921117
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.0%; Score 31; DB 1; 1 52.9%; Pred. No. 1.4e+02; tive 0; Mismatches 8;
FILING DATE: 19921117
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKEY NUMBER: 40399/134 NIHD
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
TELEFAX: 904136
TELERAX: 904136
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40399/134 NIHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/07976358 Patent No. 5445932 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 4039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                              23.0%;
50.0%;
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Best Local Similarity 50...
7; Conservative
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 25 amino acids TYPE: AMINO ACID
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AMINO ACID
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Best Local Similarity 52.9
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                            linear
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ZIP: 20007-5109
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TOPOLOGY:
US-07-976-358-15
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US-07-976-358-18
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                                                            APPLICANT: FTELDS, Howard A.
APPLICANT: KHUDYAKOV, Yuri
APPLICANT: KHUDYAKOV, Yuri
APPLICANT: FTEVOROV, Michael
TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELFA VIRUS INFECTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-976-358-15
US-07-976-358-15
Sequence 15, Application US/07976358
Fatent No. 5445932
GENERAL INFORMATION:
APPLICANT: FIELDS, Howard A.
APPLICANT: FAUDROW, Winti
TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELFA VIRUS INFECTION
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/976,358
FILING DATE: 1992117
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: BENTY Stephen A
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/976,358
  Sequence 24, Application US/07976358
Patent No. 5445932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 24 amino acids
                                                                                                                                                                                                                                                   STREET: 3000 K Street, CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3000 A CTTY: Washington, D.C.
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                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20007-5109
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Best Local Similarity
Matches 7; Conserv
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Sequence 21, Application US/07976358

Petent No. 544593

GENERAL INFORMATION:
HUDDARAL WALE

APPLICANT: FRUDYAKOV, YULI

APPLICANT: FRUDYAKOV, YULI

APPLICANT: FRUDYAKOV, WICHAE

TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER

TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER

TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER

TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER

TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER

TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER

TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER

COUNTRY: USA

ZIP: Z0007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: 19921117

CLASSIFICATION NAMBER: US/07/976,358

FILING DATE: 19921117

CLASSIFICATION NAMBER: US/07/976,358

TELERATORNEY AGENT INFORMATION:

TELERATORNEY AGENT INFORMATION:

TELERATORNEY AGENT INFORMATION:

TELERATORNEY (202)672-5309

TELERAXI (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                             LENGTH: 25 amino acids TYPE: AMINO ACID
5 YKSTVSHPDLPREVVRS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.0
Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-976-358-21
                                                                                                                             RESULT 15
US-07-976-358-21
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Search completed: August 26, 2002, 10:19:37 Job time: 393 sec

Compugen Ltd GenCore version 4.5 Copyright (c) 1993 - 2000 Comp - protein search, using sw model OM protein

August 26, 2002, 10:20:42; Search time 43.94 Seconds (without alignments) 54.671 Million cell updates/sec Run on:

25 US-09-701-623C-8 Title: Perfect score:

1 CGYGYQSIVDRPDFPKPIVRSITLC Scoring table: sedneuce:

283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext

4981 Total number of hits satisfying chosen parameters: Searched:

length: 0 length: 25 sed Minimum DB s Maximum DB s

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gene E6 protein (c tyrosine kinase su actin - mouse (fra hyroxyproline-rich T669 kinase - huma N4-(beta-N-acetylg paralytic peptide cena protein (Igal hypothetical prote histidine-rich pro ribosomal protein chlorophyll a/b-bi T-cell receptor J-endo-1,4-beta-xyla phosphoprotein pho tryptophyllin-rela extensin - maize (prote hypothetical proted(TTAGGG)n-binding Ter c gamma 1 chai 23K protein 4307 pyrrhocoricin - Py stathmin - mouse tryptophyllin-13 cytochrome-c oxida paralytic peptide paralytic peptide protein OF200051 listeriolysin O Description extensin C39855 B61079 I40692 S50900 S59485 PN0042 A05174 PA0088 B49254 PS0450 S44465 S73389 D48138 E39855 D39855 S21152 S52357 A32473 S47207 B57001 JN0910 **JP0045** Query Match Length DB 19.3 119.3 118.6 118.6 118.6 118.6 117.9 117.9 117.9 فففون 37 33 30 30 30 29 28.5 Score Result Š

paralytic peptide calotropin D1 - mu hypothetical protei hypodermin B - ear ribosomal protein translation elonga ribosomal protein ribosomal protein inbosomal protein ribosomal rotein
A39855 PT0026 S30384 A20190 A20190 JP0046 S59490 JP0048 PC0071 JP0048 E33098 E49048
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23 14 16 16 17 18 20 20 20 20 20 20 20 10 10
17.5 17.1 17.1 17.1 17.1 17.1 17.1 17.1
4 4 6 6 7 7 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9
330 331 336 336 336 344 44 34 34 34

ALIGNMENTS

C;Accession: 865374
R;Schaegger, H.; Mack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Bur. J. Blochem. 230, 235-241, 1995
Bur. J. Blochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-t
A;Reference number: 865372; MUID:95324529 cytochrome-c oxidase (EC 1.9.3.1) chain IV, cardiac - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Date: 12-Reb:1998 #sequence_revision 20-Reb-1998 #text_change 16-Jul-1999 A;Status: preliminary
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-23 <SCH>
C;Superfamily: cytochrome-c oxidase chain IV
C;Superfamily: cytochrome-c oxidase cardiac muscle; heart; oxidoreductase A; Accession: S65374 RESULT S65374

ô Gaps ô Length 23; Indels 5; Ouery Match

26.4%; Score 37; DB

Best Local Similarity 53.8%; Pred. No. 38;

Best Local Similarity 7; Conservative 1; Mismatches

3 YGYQSIVDRPDFP 15 δ

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B49254
TCR C gamma 1 chain V-J region - mouse (fragment)
TCR C gamma 1 chain V-J region - mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C.Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C.Accession: B49254
C.Accession: B49254
C.Accession: B49214

R; Ezquerra, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.Bur. J. Immunol. 22, 491-499, 1992
An'file: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of th A; Reference number: A49037; MUID:92164730
A; Reference number: A49037; MUID:92164730

A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:S90688; NID:g246308; PIDN:AAB21557.1; PID:g246309
A;Cross-references: GB:S90688; NID:g246308; PIDN:AB21557.1; PID:g246309
A;Experimental source: Y93A cells
A;Mote: sequence extracted from NCBI backbone (NCBIN:90688)
A;Mote: sequence extracted from NCBI backbone (NCBIN:90688)
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Gaps ; 0 Query Match

23.6%; Score 33; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels

1 CGYGYQS 7

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d'TTAGGG)n-binding protein B37 - human (fragment)
C.Apternate names: type A-B heterogeneous nuclear ribonucleoprotein homolog
C.Apternate names: type A-B heterogeneous nuclear ribonucleoprotein homolog
C.Apternate i6-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C.Accession: D48138
R.Ishikawa, F.; Matunis, M.J.; Dreyfuss, G.; Cech, T.R.
Moi. Cell. Biol. 13, 4301-4310, 1993
A.Fitle: Nuclear proteins that bind the pre-mRNA 3' splice site sequence r(UUAG/G) an A; Reference number: A48138; MUID:93309464
A; Status: preliminary
A; Moiteule type: protein
A; Residues: 1.17 cista
A; Residues: 1.17 cista
A; Residues: 1.17 cista
A; Residues: Heiz cell nuclei
A; Residues: Wolte: sequence extracted from NCBI backbone (NCBIP:134642)
                                             A,Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  paralytic peptide III - beet armyworm
C: Species: Spodoptera exigua (beet armyworm)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B
A:Title: Isolation and identification of paralytic peptides from hemolymph of the lep
A:Reference number: A39855; MUID:91302298
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Pred. No. 4.4e+02;
Sr. Indels
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Pred. No. 7.8e+02;
1; Mismatches 6;
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C;Species: Spodoptera exigua (beet armyworm)
                                                                                                                                                                                                     21.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Status: pre-liminary
A Molecule type: protein
A Residues: 1-23 <SKI>
C: Superfamily: paralytic peptide I
                                                                                                                                                                                      Ouery Match
Best Local Similarity 50.0
Matches 8; Conservative
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6 GSPYHWNLDRRNPDFP 21
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Best Local Similarity 38.5
Matches 5; Conservative
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Best Local Similarity 41.2
Matches 7; Conservative
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                                                                      C;Genetics;
A;Genetic code: SGC3
A;Start codon: GTG
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Especies: Pyrrhocoris apterus
C; Species: Pyrrhocoris apterus
C; Species: Pyrrhocoris apterus
C; Species: Pyrrhocoris apterus
C; Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C; Accession: S44465
B; Dupont, A: Hegy, G; Lanot, R.; Holder, F.; Hetru, C.; Hoffmann, J.A.
A; Reference number: $44463; MUID: 94271176
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
C; Function:
A; Residues: 1-20 <CCC>
C; Function:
A; Bescription: antibacterial protein
A; Note: active against Gram-negalive bacteria
C; Keywords: antibacterial; hemolymph; immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nycothetical protein A05_orf139 - Mycoplasma pneumoniae (strain ATCC 29342)
A;Variety: ATCC 29342
A;Variety: ATCC 29342
A;Variety: ATCC 29342
A;Variety: ATCC 29342
C;Species: Mycoplasma pneumoniae
C;Species: Mycoplasma pneumoniae
C;Species: A;Species: A;Species: A; At20-q449, 1996
B;Himmelreich, R; Hilbert, H; Plagens, H; Pirkl, E; Li, B.C.; Herrmann, R.
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: S73327; MUID:97105885
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;References: EMBL:AE000008; GB:U00089; NID:91673711; PIDN:AAB95715.1; PID:g167371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                               23K protein 4307 - rice (strain Nihonbare) (fragment)
C; Species: Oryza sativa (rice)
C; Species: Oryza sativa (rice)
C; Species: Oryza sativa (rice)
C; Date: 03.Feb-1994 #sequence_revision 03.Feb-1994 #text_change 11-Apr-1995
R; Tsugita, A.; Miyatake, N.
Submitted to JIPID, April 1993
A; Reference number: PS0208
A; Reference number: PS0208
A; Reference number: Sp0450
A; Molocule type: protein
A; Residues: 1-15 < TSU>
A; Residues: 1-15 < TSU>
A; Residues: 1-15 < TSU>
C; Comment: molecular weight 23K, pI 5.3.
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Pred. No. 2.8e+02;
0; Mismatches 3; Indels
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21.4%; Score 30; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels
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Best Local Similarity 66.7%;
Matches 6; Conservative
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5 SYLPRPTPPRPI 16
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1 111 1
5 CSYGYSS 11
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hypothetical protein - human
C;Species: Homo sapiens (man)
C;Access: Homo sapiens (man)
C;Accession: S2237
R;Agryrokastritis, A.; Leversha, M.A.; Ferguson-Smith, M.; Moschonas, M.K.
submitted to the EMBL Data Library, March 1993
A;Description: A cosmid clone mapped to human chromosome 11p15 detects a Taq I restri
A;Accession: S22357
A;Accession: S2257
A;Actus: preliminary
A;Wolecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-22 <AGR>
A;Cross-references: EMBL:X72881; NID:g667002; PIDN:CAA51393.1; PID:g667004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      histidine-rich protein C - liver fluke (fragment)
C;Species: Fasciola hepatica (liver fluke)
C;Date: 25-Sep-1989 #sequence_revision 12-May-1994 #text_change 15-Oct-1999
C;Accession: A32473
R;Waite, J.H.; Rice-Ficht, A.C.
Biochamistry 28, 6104-6110, 1989
A;Title: A histidine-rich protein from the vitellaria of the liver fluke Fasciola hep A;Reference number: A32473; MUD:89375343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to JIPID, February 1994
A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal
A;Reference number: JP0042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Wolecule type: protein
A;Residues: 1-23 < WAI>
A;Note: 22-G1y, 22-Ser, 23-G1y, and 23-Ser were also found
C;Keywords: egg yolk
F;6,8,12,16/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental
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C;Species: Staphylococcus aureus
C;Accesion: JP0044 #sequence_revision 28-oct-1994 #text_change 03-May-1996
C;Accesion: JP0045
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Pred. No. 9.3e+02;
0; Mismatches 1; Indels
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C;Superfamily: Escherichia coli ribosomal p
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                     20.0%;
66.7%;
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ilarity 83.3%;
Conservative
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 5; Conserv
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1 MDRPDY 6
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C; Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993 C; Accession: D39855 R; Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B. A; Biol. Chem. 266, 12873-12877, 1991 A; Title: Isolation and identification of paralytic peptides from hemolymph of the lepide A; Reference number: A39855; MUID:91302298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tryptophyllin-related peptide - two-colored leaf frog
C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Accession: 221152
C;Accession: 221152
R;Mignogna, G; Severini, C; Simmaco, M; Negri, L; Falconieri Erspamer, G; Kreil, (FBS Lett. 302, 151-154, 1992
A;Title: Identification and characterization of two dermorphins from skin extracts of A;Reference number: $21152; MUID:92339502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                extensin - maize (fragment)
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: 833609
R;Murphy, J.M.; Hood, E.E.
R;Murphy, J.M.; Hood, E.E.
A;Title: Molecular basis for extensin size heterogeneity in two maize varieties.
A;Reference number: 833609; MUID: 93222485
A;Accession: 833609
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Pred. No. 4.9e+02;
3; Mismatches 2;
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42.1%; Pred. No. 6.7e+02;
Live 1; Mismatches 2;
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Pred. No. 7.8e+02;
L; Mismatches 6;
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A;Residues: 1-17 <MUR>
C;Keywords: glycoprotein; hydroxyproline
                                                                                                                                                                           A;Status: preliminary
Modecule type: protein
A;Residues: 1-23 <SKI-
C;Superfamily: paralytic peptide I
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Similarity 41.2%;
7; Conservative
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Best Local Similarity 42.18
Matches 8; Conservative
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Best Local Similarity
'-haq 4; Conserv?
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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2 EKPFYPPPI 10
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Gaps

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Indels

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B5/001
endo-1,4-beta-xylanase (EC 3.2.1.8) 2 - Streptomyces roseiscleroticus (fragment)
C;Species: Streptomyces roseiscleroticus
C;Date: 03-oct-1995 #sequence_revision 03-oct-1995 #text_change 06-bec-1996
C;Accession: B5705 #sequence_revision 03-oct-1995 #text_change 06-bec-1996
C;Accession: B5706 # 120-129, 1993
A;Title: Characterization and N-terminal amino acid sequences of beta-(1-4)endoxylanases
A;Reference number: A57001; MUID:93229899
A;Reference number: A57001; MUID:93229899
A;Reference number: B57001
A;Residues: Declaininary
A;Molecule type: protein
A;Residues: 1-25 <GRA>
A;Residue
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                                                                                                                                                                                                                                                                                                                                            T-cell receptor J-alpha wnVIII.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S47207
R; Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
submitted to the EMBL Data Library, February 1993
A; Reference number: S40133
A; Reference number: S40133
A; Reference number: S40133
A; Reterence number: A1207
A; Status: preliminary
A; Roslecule type: mRNA
A; Residues: 1-21 <PLA>
A; Residues: 1-21 <PLA>
A; Cross-references: EMBL:X71032; NID:g506610; PIDN:CAA50349.1; PID:g510318
C; Keywords: T-cell receptor
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19.3%; Score 27; DB 2; Length 21;
Best Local Similarity 55.6%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 3; Indels
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19.3%; Score 27; DB 2; Length 25;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 6; Indels
                                                              9 RSVIGRPETORKIVEAL 25
6 QSIVDRPDFPKPIVRSI 22
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10 SLVPEPDCP 18
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Search completed: August 26, 2002, 10:20:42 Job time: 348 sec

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Mon Aug 26 11:09:39 2002
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August 26, 2002, 10:30:18; Search time 22.95 Seconds (without alignments) 42.178 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                   OM protein - protein search, using sw model
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US-09-701-623C-8 140 1 CGYGYQSIVDRPDFPKPIVRSITLC 25 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

105224 seqs, 38719550 residues Searched:

1503 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 25

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P80410 palomena pr			palomena	pyrrhocor			P30257 spodoptera					P82660 panagrellus						P80906 methanobact	P81674 pinus pinas	P12663 ovis aries	P01021 agkistrodon	4	P08613 kassina mac	P58025 chlorobium	P05975 halobacteri	P36503 streptomyce	7	P37046 streptomyce	P56684 androctonus	3	889	P22800 apanteles k
SUMMAKIES		ID	MK2B_PALPR	MK1_PALPR	MK2A_PALPR	MK3_PALPR	PYRR_PYRAP	CP23_SPOER	PAP2_SPOEX	PAP3_SPOEX	TP13_PHYRO	PAP1_SPOEX	CAMT_PINPS	PAP1_MANSE	FAR6_PANRE	CAL1_CALGI	YMOR_PSEPU	UP21_UPEIN	UP24_UPEIN	FRE4_LITIN	KORC_METTM	UN05_PINPS	IRBP_SHEEP	BPPB_AGKHA	GRAR_RANRU	TKN1_KASMA	RUBR_CHLTE	RL23_HALCU	DURC_STRGP	LPRM_CORDI	RP71_STRSQ	ANDT_ANDAU	CXA4_CONPU	~	GBP_APAKA
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		Length	16	15	15	16	20	23	23	23	13	23	24	23	10	14	16	19	19	24	20	20	24	11	12	12	17	18	19	21	21	25	25	24	25
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P14596 tabanus atr P28467 acinetobact	P80155 Theromyzon P19633 rattus norv P81241 carica papa P12662 sus scrofa	P30254 manduca sex P81173 streptomyce P82098 litoria rub P54712 canis famil	P01521 conus magus P80907 methanobact
HTF_TABAT ACEA_ACICA	HEMH_THETS CAQS_RAT CHLY_CARPA IRBP_PIG	PAP2_MANSE BLAC_STRGR EI22_LITRU SODM_CANFA	CXA1_CONMA VORA_METTM
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21	2112	20. 20 20 20 20	50 20 20
3.54	35 38 39	40 43 43	44 45

ALIGNMENTS

MK2B_PALPR ID MK3B_PALPR ID MK3B_PALPR To P8410; To 1.40V-1995 (Rel. 32, Created) DT 01.NOV-1995 (Rel. 32, Last sequence update) DT 01.NOV-1995 (Rel. 32, Last sequence update) DT 01.NOV-1995 (Rel. 36, Last annotation update) DE Mctalnikowin IIB. OS Palomena prasina. OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera; OC Pterygota; Neoptera; Paraneoptera; Pentatomomorpha; Pentatomoidea; OC Pterygota; Neoptera; Paraneoptera; Pentatomomorpha; Pentatomoidea; OC Pterygota; Neoptera; Pantatomona. NCBL_TaxID=55431; RN [1] RN [1] RA (TISSUE-Hemolymph; RA	QY 9 VDRPDF-PKPIVRSI 22
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ISSUE-Hemolymph;
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"The inducible antibacterial peptides of the hemipteran insect
Palomena prasina. Identification of a unique family of proline-rich
peptides and of a novel insect defensin.";
J. Insect Physiol. 42.81-89(1996).
-I- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
1;
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomoidea;
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Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomoidea;
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                                                                                                                        Indels
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                                           BACTERIA.
-1- INDUCTION: BY BACTERIAL INFECTION.
Antiblotic; Insect immunity. 21407E663CE46299 CRC64;
SEQUENCE 15 AA; 1838 MW; 21407E663CE46299 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           Antibiotic; Insect immunity.
SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;
                                                                                                       DB 1;
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                            (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 36, Last annotation update)
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                                                                                                              Pred. No. 40;
3; Mismatches
                                                                                                       Score 33.5;
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60.0%;
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NCBI_TaxID=55431;
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Best Local Similarity
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1 VDKPDYRPRP 10
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TISSUE-Hemolymph;
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P80409;
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P80411;
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                                                                                                                                                                                                                                                                                            Gaps
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Chernysh S., Coctancich S., Briand J.-P., Hetru C., Bulet P.;
"The inducible antibacterial peptides of the hemipteran insect
Palomena prasina. Identification of a unique family of proline-rich
peptides and of a novel insect defensin.";
J. Insect Physiol. 42.81-89(1996).
--- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
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P37362; P801307;
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pyrrhocoricin.
Pyrrhocoricin.
Byrrhocoris Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neptera; Paraneoptera; Hemiptera; Euhemiptera; Phenryoptera; Panheteroptera; Pentatomomorpha; Lygaeoidea;
                                                                                                                                                                                                                                                    Score 33.5; DB 1; Length 16; Pred. No. 43;
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                                                                                                                    BACTERIA,
-!- INDUCTION: BY BACTERIAL INFECTION.
Antiblotic; Insect immunity. A9E3835D063B9462 CRC64;
SEGUENCE 16 AA; 2024 MW; A9E3835D063B9462 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
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20 AA; 2341 MW; F4320EC2FF29462C CRC64;
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                                                                                                                                                                                                                                                                                        3; Mismatches
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Biochem. J. 300:567-575(1994).
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MEDLINE-94271176; PubMed-8002963;
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50.0%;
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NCBI_TaxID=37000;
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SYLPRPTPPRPI 16
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Matches 6; Conserv
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Matches 6; Conserv
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Andrew Village Street

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Pfam; PF02425; GBP_PSP; 1.
                  Hemolymph.
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SEQUENCE
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P30257;
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                                                                                                                               Query Match
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J. Biol. Chem. 266:12873-12877(1991).

-I-FUNCTION: CAUSES RAPID. RIGID PARALYSIS WHEN INJECTED INTO LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.

-I-SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY. PIR, D39855; D39855.

HSSP; 061704; 1B5N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARIY: DELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY. HSSP; OG1704; 185N. InterPro; IPR03463; GBP_PSP. Pfam; PF02425; GBP_PSP; 1. BY SIMILARIMY.
                                                                                                                                                   Cardioactive peptide CAP23.
Spodoptera eridanta (Southern armyworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Nocuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides 20:53-61(1999).
-I- FUNCTION: HAS EXCITATORY EFFECTS ON A SEMI-ISOLATED HEART FROM LARVAL MANDUCA SEXTA, CAUSING AN INOTROPIC EFFECT AT LOW CONCENTRATIONS OF PEPTIDE AND CHRONOTROPIC AND INOTROPIC EFFECTS
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctucidea; Noctuidae; Amphipyrinae; Spodoptera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                      MEDLINE-99196260; PubMed-10098624; Furuya K., Hackett M., Cirelli, M.A., Schegg K.M., Wang H., Shabanowitz J., Hunt D.F., Schooley D.A.; Shoorive Peptide from the southern armyworm, Spodoptera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
0A96D72A70855AE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28.5; DB 1;
Pred. No. 3.6e+02;
; Mismatches 6;
                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
12-UL-1999 (Rel. 38, Last annotation update)
Paralytic peptide II (PP II).
                                                             23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 AA
                                                             PRT;
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23 AA; 2519 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 20.4
Best Local Similarity 41.2
Matches 7; Conservative
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                                                           STANDARD;
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                                                      CP23_SPOER
P56683;
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SEQUENCE.
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                                      CP23_SPOER
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PAP2_SPOEX
               RESULT
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J. Blol. Chem. 266:12873-12877(1991).

-I. FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
-I.EPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
-I. STMILARLIY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY. PIR: 539855; E39855.
                                                                                                                                Gaps
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neopiera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctucidea; Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phyllomedusa rohdei (Rohde's leaf frog).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Phyllomedusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Hemolymph;
MEDLINE-91302298; PubMed-2071576;
Skinner W S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
Quistad G.B.;
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                                                                                     Length 23;
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BY SIMILARITY.
0A96CB4600855AE0 CRC64;
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                                                                                     Score 28.5; DB 1;
Pred. No. 3.6e+02;
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Pred. No. 3.6e+02;
L; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
12-UL-1999 (Rel. 38, Last annotation update)
Paralytic peptide III (PP III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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                                                                                                                              1; Mismatches
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  19
2477 MW;
                                                                                   20.4%;
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Pfam; PF02425; GBP_PSP; 1.
Hemolymph.
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Best Local Similarity 41...
7; Conservative
                                                                                                                                                                      1 CGYGYQSIVD---RPDF 14
                                                                                                                                                                                                            7 CIPGYORTADGRCKPIF 23
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                                                                                                                                7; Conservative
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                                                                                                   Best Local Similarity
Matches 7; Conserv
  7
23 AA;
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TISSUE-Needle;
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P30253;
                                                                                                                                                                                                                 proteins."
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                         the lepidopteran insects Manduca Sexta, Spodoptera exigua, and Hellothis virescens.";
J. Biol. Chem. 266:12873-12877(1991).
- FIOLOTTON: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
-!- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY. PIR: C39855; C39855.
                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUJ-1999 (Rel. 38, Last annotation update)
Paralytic peptide I (PP I).
Spodoptera exigua (Beet armyworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota; Meoptera; Endopterygota; Lepidoptera;
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
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                 Montecucchi P.C., Gozzini L., Erspamer V.;
"Primary structure determination of a tryptophan-containing tridecapeptide from Phyllomedusa rohdei.";
Int. J. Pept. Protein Res. 27.175-182(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26, DB 1; Length 23; Pred. No. 8.7e+02; Mismatches 5; Indels
                                                                                                                   Score 26; DB 1; Length 15;
Pred. No. 4.7e+02;
Transfels 2; Indels
                                                                                      PYRROLIDONE CARBOXYLIC ACID. 33BF33A212227773 CRC64;
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0A96D1F600855AE0 CRC64;
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                                                                                                                                                                                                                                  23 AA
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(Rel. 36, Last sequence update)
                                                                                                                                                                                                                                  PRT;
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InterPro; IPR003463; GBP_PSP.
Pfam; PF02425; GBP_PSP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.6%;
50.0%;
                                                                                                                           18.68;
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2451 MW;
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13 AA; 1646 MW;
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Best Local Similarity 44.۰۰
امر 4; Conservative
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                                                                                                                                                                                                                                  STANDARD;
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                                                                PIR; A05174; A05174
Amphibian skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
23 AA;
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGYGYQSIVD 10
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TISSUE-Hemolymph;
                                                                                                                                                                           ::| :| || || 2 EKPYWPPPI 10
                                                                                                                                                                 10 DRPDFPKPI 18
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P8\(\frac{1}{2}\)(81;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hemolymph.
DISULFID
SEQUENCE
                                                                                                                                                                                                                                 PAP1_SPOEX P30255;
 [1]
SEQUENCE.
                                                                                     MOD_RES
SEQUENCE
                                                                                                                                                                                                               RESULT 10
PAP1_SPOEX
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-I- FUNCTION: INVOLVED IN THE REINFORCEMENT OF THE PLANT CELL WALL UNDER CONDITIONS THAT TRIGGER THE DISEASE RESISTANCE RESPONSE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 28, Last annotation update)
Paralytic peptide I (PP I)
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neopera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Sphinglodea: Sphinglae; Sphinglae; Manduca.
                                                       caffeoyl-CoA 3-O-methyltransferase) (CCOAMT) (CCOAOMT) (Water stress responsive protein 13) (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + caffeoyl-CoA - S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from hemolymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adenosyl-L-homocysteine + feruloyl-COA.
--- PATHMAY: LIGNIN BIOSYNTHESIS.
--- SUBUNIT: HOMODIMER (BY SIMILARITY).
--- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS: 5.2, ITS MW IS: 30 kba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plomion C.; "Separation and characterization of needle and xylem maritime pine
                                                                                                            Pinus pinaster (Maritime pine).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
NCBI_TaxID=71647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
30-WAY-2000 (Rel. 39, Last annotation update)
Probable caffeoyl-COA O-methyltransferase (EC 2.1.1.104) (Trans-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation and identification of paralytic peptides from hemoly the lepidopteran insects Manduca sexta, Spodoptera exigua, and Heliothis virescens.", 15 Biol. Chem. 266:12873-12877(1991).
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                                                                                                                                                                                                                                                                                                                                                                                Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.; "Water-deficit-responsive proteins in maritime pine."; Plant Mol. Biol. 38:587-596(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26; DB 1; Length 24; Pred. No. 9.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Needle;
MEDLINE-99274088; PubMed=10344291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Hemolymph;
MEDLINE-91302298; PubMed-2071576;
                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98418576; PubMed-9747804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2447 MW;
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Similarity 44.4%;
4; Conservative
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24 AA;
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Best Local Similarity
Matches 4; Conserv
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Pseudomonas.
NCBI_TaxID=303;
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LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
-1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
HSSP: O61704; 185N.
                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation, characterization and pharmacology of RMRFamide-related peptides (FBRFPS) from free-living nematode, Panagrellus redivivus."; Submitted (JUL-2000) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 34.22.-) (Fragment).
Calotropin 91gantea (Madar) (Bowstring hemp).
Eukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Apocynaceae; Asclepiadoideae; Asclepiadoideae; Nost_TaxID=4066;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, FUNCTION, AND AMIDATION.
Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó.
                                                                                                                                                    3;
                                                                                                                             Score 24.5; DB 1; Length 23;
Pred. No. 1.5e+03;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24; DB 1; Length 10;
Pred. No. 7.2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Panagrolaimidae; Panagrellus.
                                                                                    BY SIMILARITY.
0B26CB5C29855FE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION.
CB13E4C9D776C76D CRC64;
                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
                                                                                                                                                                                                                                                 10 AA.
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                                                  InterPro: IPR003463; GBP_PSP.
Pfam; PF02425; GBP_PSP; I.
Hemolymph. 7 19 1
                                                                                                                               17.5%;
                                                                                    19
2436 MW;
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10 AA; 1132 MW;
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                                                                                                                                                    Conservative
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23 AA;
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                   9;
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P20728:
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93199531; PubMed=8452544; Willey D.L., Caswell D.A., Lowe C.R., Bruce N.C.; Willey D.L., Caswell D.A., Lowe C.R., Bruce N.C.; Nucleotide sequence and over-expression of morphine dehydrogenase, a plasmid-encoded gene from Pseudomonas putida M10."; Blochem. J. 290:539-544(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 24; DB 1; Length 14; 60.0%; Pred. No. 1e+03;
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Pred. No. 1.2e+03;
2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                           D993F0276CDA4662 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hyporhetical protein in MORA 3 region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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Hypothetical protein; Plasmid.
NON_TER 16 16
SEQUENCE 16 AA; 1962 MW: A
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40.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Conservative
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Matches 6; Conservative
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Plasmid pMDH7.2.
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09x368 prochloroco 09x396 prochloroco 09x352 prochloroco 09z355 chlamydia t 013659 homo sapien 091kc7 hepatitis c

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ALIGNMENTS

SEQUENCE FROM N.A.
Urbach E., Chisholm S.W.;
Urbach E., Chisholm S.W.;
Urbach E., Chisholm S.W.;
Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";
Limnol. Oceanog. 43:1615-1630(1998).
Limnol. AF070158; AAD23203.1; -.
SEQUENCE 21 AA; 2340 MW; CC947A36F12C854F CRC64; Gaps ö Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaee; Prochlorococcus. NCBI_TaxID=1220; 25.0%; Score 35; DB 2; Length 21; 46.7%; Pred. No. 1.5e+02; Live 3; Mismatches 5; Indels 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT). 21 AA. Query Match 25.C Best Local Similarity 46.7 Matches 7; Conservative ||::|| |:|| 2 SILKKPDLTDPKLRS 16 7 SIVDRPDFPKPIVRS 21 Prochlorococcus sp. Q9X3G4 RESULT Q9X3G4 ŏ Q

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Created) Last sequence update) 25 AA PRT; 067969 PRELIMINARY; 067969; 01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, RESULT 067969 DA DA

OM protein

Run on:

August 26, 2002, 10:29:35

US-09-701-623C-8

140 1 CGYGYQSIVDRPDFPKPIVRSITLC Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 25

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPIREMBL_19:*
1: sp_archea:*
2: sp_bacteria:* Database

sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:* sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_phage:* sp_plant:* sp_rodent:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rvirus:* sp_bacteriap:*

sp_archeap:*

SUMMARIES

Description	00000	067969 prochloroco	Ogyafa prochlored	0001011001d 216464	005638 ptlemmona	OSWYS DICCHIOLICAN	Ogmbhs strontococ	000000 101100000	OSEANS TALLED SP.	Cook as the teak	056610 wihrio obol	1000 OTTAL VIOLE CONDE		Q9x3nU prochloroco	O9x3i8 prochloroco			Oguce/ nomo sapien
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Query Match	25.0	24.3	23.6	23.6	23.6	22.9	22.9	22.9	22.9	22.1	22.1	22.1	22 1		71.4	21.1	20.7	
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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SVTKKPDLTDPVLKA 16
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2 SVIKKPDLSDPRLRA 16
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
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                       NCBI_TaxID-1220;
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              Prochlorococcus
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                                                                                                       STRAIN-MIT9303;
MEDLINE-98123172; PubMed-8452521;
MEDLINE-98123172; PubMed-8452521;
Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;
Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;
"Rapid diversification of marine picophytoplankton with dissimilar
light-harvesting structures inferred from sequences of Prochlorococcus
and Synechococcus (Cyanobacteria).";
J. Mol. Evol. 46:188-201(1998).
N. Mol. Evol. 46:188-201(1998).
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Urbach E., Chisholm S.W.;
Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";
Limnol. Oceanog. 43:1615-1630(1998).
EMBL; AF070149; AAD20770.1; -.
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                             Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae; Prochlorococcus.
                                                                                                                                                                                                                                         Score 34; DB 2; Length 25;
Pred. No. 2.6e+02;
4; Mismatches 4; Indels
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
C#TOCHROME B6/F COMPLEX SUBUNIT IV (FRACMENT).
PHTD.
                                                                                                                                                                                                            504CCD63AC947A21 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
    01-DEC-2001 (TrEMBLrel. 19, Last annotation update) B6/F COMPLEX SUBUNIT IV (FRAGMENT).
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Pred. No. 3e+02;
5; Mismatches
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Best Local Similarity 33.3
Matches 5; Conservative
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2 SVIKKPDLEDPKLRA 16
                                       rochlorococcus marinus
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3 ILKKPDFSDPKLRA 16
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Best Local Similarity
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                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prochlorococcus.
NCBI_TaxID=1220;
                                                                       NCBI_TaxID-1219;
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SEQUENCE
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SEQUENCE
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Q9X3G0;
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Matches
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Q9X3G0
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Q9X3F2
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                                        populations flow cytometrically Stream.";
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NCBI_TaxID=163303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Gohalmi S.E., Huner N.P.A.; Gudynaite-Savitch L., Kohalmi S.E., Huner N.P.A.; Structural analysh of cytochrome f from the psychrophilic alga Chlamydomonas subcaudata.";
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                          Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY039799; AAK64210.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 23 23 23 SEQUENCE 23 AA; 2429 MW; F255B6AE00DA2134 CRC64;
                                                                                                                                                                   21 AA; 2324 MW; D3AFDAECFA34E54F CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) CYTOCHROME B/F COMPLEX SUBUNIT IV (FRAGMENT).
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Pred. No. 3.3e+02;
5; Mismatches 5;
                                                                                                                                                                                                                                     23.6%; Score 33; DB 2;
33.3%; Pred. No. 3e+02;
iive 5; Mismatches
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SEQUENCE FROM N.A.
Urbach E., Chisholm S.W.;
Urbach E., Chisholm S.W.;
Genetic diversity in Prochlorococcus
sorted from the Sargasso Sea and Gulf
Limnol. Oceanog. 43:1615-1630(1998).
BEBL; AF070155; AB020780.1;
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26.7%;
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Q95E38;
01-DEC-2001 (TFEMBLEE). 19,
01-DEC-2001 (TFEMBLEE). 19,
01-DEC-2001 (TFEMBLEE). 19,
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Gaps

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Length 22;

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Eukaryota; Viridiplanta; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Majnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stephens R.M.;
"Expression of the bovine leukemia virus X region in virus-infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
STRAIN-CV. DE GRACE; TISSUE-LERE;
MEDLINE-20181728; Pubmed-10715320;
Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
Adamska I., van Wijk K.J.;
"Proteomics of the chloroplast: systematic identification and
targeting analysis of lumenal and peripheral thylakoid proteins.";
Plant Cell 12:319-341(2000).
-: SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
-: DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=87198886; PubMed=3033284;
Rice N.R., Simek S.L., Dubois G.C., Showalter S.D., Gilden R.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.9%; Score 32; DB 15; Length 23; 50.0%; Pred. No. 4.8e+02;
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF THYLAKOID LUMEN (SPOT204)
                                                                                                                                                                                                                Score 32; DB 11; Length 22
Pred. No. 4.5e+02;
5; Mismatches 5; Indels
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Bovine Leukemia virus (BLV).
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
NCBI_TaxID=11901;
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NON_TER 23 AA; 2877 MW; F85E7CBED5440B08 CRC64;
                                                                                                                                                            22 AA; 2407 MW; B82830E4477E25F9 CRC64;
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Last annotation update)
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                                                                                                    InterPro; IPR001580; Calreticulin.
Pfam; PF00262; Calreticulin; 1.
ProDom; PD001866; Calreticulin; 1.
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28.6%;
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                                                                                                                                                                                             Ouery Match
Best Local Similarity 28.0
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Matches 5; Conservative
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Q85496;
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...uach E., Chisholm S.W.;
"Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";
Elmol. Oceanog. 43:1615-1630(1998).
EMBL; AF070172; AAD20786.1; -.
EMBL; AF070172; AD20788.1; -.
NON_TER
21
SEQUENCE 21 **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-20392133; PubMed-10933687;
Gindraau E., Lopez R., Garcia P.;
Gindraau E., Lopez R., Garcia P.;
*Mul, a temperate bacteriophage of the type 23F Spanish/USA
multiresistant epidemic clone of Streptococcus pneumoniae: structural
analysis of the site-specific integration system.";
J. Virol. 74:7803-7813(200)
EMBL; AJ400632; CAB96625.1;
EMBL; AJ400629; CAB96617.1;
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                Gaps
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=120574;
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"Identification and purification of a calcium-binding protein in hepatic nuclear membranes.";
J. Biol. Chem. 268:4291-4299(1993).
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                                                                                                                                                                                                                                                                                      Score 32; DB 2; Length 21;
Pred. No. 4.3e+02;
4; Mismatches 5; Indels
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CELL WALL LYTIC ENZYME (FRAGMENT).
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Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequen
01-JUN-2001 (TrEMBLrel. 17, Last annota
P93 CALCIUM-BINDING PROTEIN (FRAGMENT).
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Matches 6; Conserv
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Matches 5; Conser
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3 SMADKPDF 10
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SEQUENCE
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RESULT Q9MBH5

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Q9X3J8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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Eukaryota (Pig)
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                Score 31; DB 10; Length 14;
Pred. No. 4e+02;
2; Mismatches 1; Indels
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"Regulation of VSMC Differentiation.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF330200; AAL09466.1;
Chloroplast; Thylakoid membrane.
NON_TER 14 14
SEQUENCE 14 AA; 1505 MW; 2EABFAF980F3D7D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 175:281-283(1996).
EMBL; U30472; AAC44579.1; -.
NON_TER 18 18
SEQUENCE 18 AA; 2153 MW; 18EBCDAD212842EF CRC64;
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095JA2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last senocation update)
INTEGRIN ALPHA 2 SUBUNIT (FRAGMENT).
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Last annotation update)
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                                                                                                       Query Match 22.1%;
Best Local Similarity 62.5%;
Matches 5; Conservative
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Matches 6; Conservative
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TISSUE-CARDIOVASCULAR;
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                                                                                                                                                                                          4 GYQSIVDR 11
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4 GFQPVVDR 11
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Urbach E., Chisholm S.W.;
Urbach E., Chisholm S.W.;
Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";
Limnol. Oceanog. 43:1615-1630(1998).
EMBL; APO70163; ADD2312:1.;
NON_TER
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SEQUENCE 21 AA; 2280 MW; CC946C4A2034E54F CRC64;
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Urbach E., Chisholm S.W.;
Urbach E., Chisholm S.W.;
Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";
Limnol. Oceanog. 43:1615-1630(1998).
EMBL: AR7070199; AD22328.1; -..
21 21 21
SEQUENCE 21 AA; 2298 MW; CC946FFCC02C854F CRC64;
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Bacteria; Vanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
NCBL_Tax1D=1220;
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Bacteria; Vanobacteria; Prochlorophytes; Prochlorococcacea;
Prochlorococcus.
NCBL_TaxID=1220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 2; Length 21; Pred. No. 6.1e+02; 5; Mismatches 5; Indels
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
Score 31; DB 6; I
Pred. No. 5.2e+02;
2; Mismatches 4;
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Best Local Similarity 33.3%;
Matches 5; Conservative 5
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2 SVLKKPDLADPKLRA 16
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2 STLKKPDLADPKLRS 16

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21.1%; Score 29.5; DB 5; Length 24;
54.5%; Pred. No. 1.2e+03;
Live 3; Mismatches 1; Indels 1; Gaps
                                                                                                                                                                                                  P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

TRANSPOSON-GRT-G6 BUBMEd=11121049;

A Arkhipova I., Meselson M.;

Transposable elements in sexual and ancient asexual taxa.";

Transposable elements in sexual and ancient asexual taxa.";

Proc. Natl. Acad. Sci. U.S. A. 97:14473-14477 (2000).

R EMBL; AY013996; AAG5968.1;

W RN-directed DNA polymerase.

NON_TER 24 24

NON_TER 24 24

SEQUENCE 24 AA; 2499 MW; 4A03DE8E3F7A4D12 CRC64;
                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GYPSY-LIKE REVERSE TRANSCRIPTASE (FRAGMENT).
Spongilla lacustris (Freshwater sponge).
BURATYOLS; Metazoa; Porifera; Demospongiae; Ceractinomorpha; Haplosclerida; Spongillidae; Spongilla.
                                   24 AA.
                                   PRT;
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Best Local Similarity 54.5
Matches 6; Conservative
                                 PRELIMINARY;
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RESULT 15
Q9BM10
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Search completed: August 26, 2002, 10:29:35 Job time: 650 sec

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- protein search, using sw model OM protein

August 26, 2002, 10:18:42; Search time 79.43 Seconds (without alignments) 34.960 Million cell updates/sec Run on:

US-09-701-623C-8 140 1 CGYGYQSIVDRPDFPRPIVRSITLC Title: Perfect score: Sequence:

25

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues Searched:

253524 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 25

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

1. (SIDS)/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT: *
2. (SIDS)/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT: *
3. (SIDS)/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT: *
4. (SIDS)/gcgdata/hold-geneseqy-embl/AA1982.DAT: *
5. (SIDS)/gcgdata/hold-geneseqy-embl/AA1985.DAT: *
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6. (SIDS)/gcgdata/hold-geneseqy-embl/AA1985.DAT: *
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22. (SIDS)/gcgdata/hold-geneseqy-embl/AA2001.DAT: *
22. (SIDS)/gcgdata/hold-geneseqy-embl/AA2001.DAT: * A_Geneseq_032802:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	CHOLUMN TAREST CHO	Optimised 198 Ch3	Optimised 19E-CH3	Optimized 19E-Cas	Optimised 19E-Ch3	Modified himse ten	Dontide feminal 19E	reputate sequence o	AULIDOGY 15A.2 mur	Antibody 15A.2 swi	Peptide which bind	Antibody 15A.2 bin
SUMMARIES	a	AAY80001	AAX80000	AAY80077	AAY79999	AAY79998	AAY91212	AAY68602	AAYSORGE	000003444	96900144	AAR02179	AAY50893
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	Ouery Match Length DB	25	25	25	25	25	25	25	15	17	ì ;	/1	17
æ	Ouery Match	100.0	75.7	52.9	47.1	45.7	45.7	45.7	38.6	37 9		32.I	29.3
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Antibody 15a 2 can	15A 2 fe	נטטעוושש	Proline-rich antih	401.1	۰,	ohrenia-	•	Sequence of pentid		SH3 domain-binding		midd	de de	Type I polyketide	۲.		Branched peptide C	Antibody 15A 2 are		ਾਹ	lass II	class II	្ព	PPPPY motif contai	u	NS5 protein	NS5 protein	atitis C viru	ا ت د	ded		nentide XVIII	atitis C vir
AAY50894	AAY50897	AAW24102	AAW09376			AAU25118	AAU15462		AAW05484	AAW05416	AAW16970	AAW25345	AAW09377	AAB20671	AAR41158	AAW17451	AAR51405	AAY50896	AAW59655	AAB88089	AAY98820	AAY98912	AAW05469	AAW37677	AAR41190	AAR41191	AAR41192	AAW10148	AAW10149	AAY58800	AAR41118	AAR41119	
21	21	18	17	17	22	22	22	14	17	17	17	18	17	21	14	17	15	21	19	22	21	21	17	18	14	14	14	18	18	21	14	14	16
17	17	20	16	18	12	12	12	16	20	20	20	20	16	17	22	11	17	17	14	14	15	15	18	18	20	20	20	20	20	21	22	22	23
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12	13	14	15	16	17	18	19	20	21	22	23	7.4	25	56	27	28	59	30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	

ALIGNMENTS

RESULT AAY80001

Ą. AAY80001 standard; Peptide; 25

AAY80001;

(first entry) 15-MAY-2000 Optimised IgE-CH3 domain antigen peptide for mouse IgE.

Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthmati; dermatitis.

Mus sp. Synthetic.

WO9967293-A1.

29-DEC-1999

99WO-US13959. 21-JUN-1999;

98US-0100287. 20-JUN-1998;

(UNBI-) UNITED BIOMEDICAL INC.

Wang CY, Walfield AM;

WPI; 2000-160578/14.

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy \cdot

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antigence invention userines immunicationin to the present antibodies and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of 1gE, and so preventing triggering and activation of mast cells and basophils and so preventing triggering and activation of mast cells and basophils containing (I) are used for active immunisation against 1gE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints disaulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe maximize cross-reactivity to the natural target. They induce safe acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
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                                              the present invention describes immunoglobulin E (IgE)-CH3 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 25;
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100.0%; Pred. No. 7.9e-15;
iive 0; Mismatches 0;
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             Claim 1; Page 100; 155pp; English.
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          and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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specific for a target effector site on the epsilon-heavy chain of IgE
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                                                                                                                                                                                                                                                                                                                                                            75.7%; Score 106; DB 21;
80.0%; Pred. No. 1.6e-09;
iive 0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-160578/14.
                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                         25 AA;
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                                                                                                                                                                                                                                                                                                           Sednence
                                                                                                                                                                                                                                                                                                                                                                Query Match
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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyglomal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and so preventing triggering and activation of mast cells and basophils. Containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous Thelper cell epitope. Conjugates of in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe
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recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (1) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent anino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.9%; Score 74; DB 21; Length 25; 52.0%; Pred. No. 0.00015; Live 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Optimised IgE-CH3 domain antigen peptide for dog IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGYGYQSIVDRPDFPKPIVRSITLC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for immunization against allergy
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                              25 AA;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                              Sequence
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(non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobulic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
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                                                                                                                                                  Gaps
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                                                                                                            Score 66; DB 21; Length 25;
Pred. No. 0.0027;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Optimised IgE-CH3 domain antigen peptide for human IgE.
                                                                                                                                                                                                                                                                                                                       ¥.
                                                                                                                                                                                     1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                           Claim 1; Page 21; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for immunization against allergy
                                                                                                                                                                                                                                                                                                                   AAY79998 standard; Peptide; 25
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                                                                                                              47.1%;
56.0%;
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                            Query Match 47.1
Best Local Similarity 56.0
Matches 14; Conservative
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                                                          Sequence
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The invention relates to novel promiscuous T helper cell epitopes (Th), along with B cell epitopes. The Th epitopes of the invention along with B cell epitopes. The Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, pertein (EFTP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer infections (HRY) for contraception, treatment of hormone releasing hormone (LHRH) for contraception, treatment of hormone capendant cancer, prevention of boar taint in meat, and immunocastration); for promoting the growth of animals; or for treating allergies or arteriosciences. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antipen. The contrace of antibodies against a target antipen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epitopes. Sequence AAY91121 represents a promiscuous T helper epitope frâm the measles virus F (MVF) protein and sequences AAY91122- V91142, AAY91226 and AAY91246 represent synthetic Th epitopes based on the MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
                                                                                                                                                                                                                                                                                                                                                                               Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic; Plasmodium falciparum; circumsporozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus
                                            Gaps
                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVF Th epitope. Sequence AAYVII43 Teptesents of From--
from hepatitis B virus (HBV) surface antigen, and sequences
Score 64; DB 21; Length 25;
Pred. No. 0.0055;
                                          Indels
                                          10;
                                                                                                                                                                                                                                                                                                                                                Modified human IgE CH3 domain, SEQ ID NO:92.
                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 40; 129pp; English.
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                                                                               1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                      AAY91212 standard; peptide; 25
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  45.7%;
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                                          Conservative
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                Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                              AAY91212;
    Query Match
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AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
AAY91156-Y91196, AAX91227 and AAX91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
is the LHRH target antigenic peptide used in these LHRH antigenic
peptides comprising somatostatin, and AAY91201-Y91207 are antigenic
peptides comprising somatostatin, and AAY91201-Y91207 are antigenic
cpeptides comprising somatostatin and a Th epitope. Somatostatin
cimmunogens may be used to promote growth in livestock. AAY91208 is a
human CD4 CDR2 antigenic peptides which may be used to prevent HIV
ciffection of T cells. AAY90212 is a modified version of a human IgE
confidence peptides which may be used in the treatment of allergies.
AAY91220 is a peptide which may be used in the treatment of allergies.
AAY91221 is a plasmoddum falciparum circumsporzozite (CS) target
antigen, and AAY91221 se and AAY91231-Y91222 comprise this peptide and Th AAY91235 comprise the immunogens comprising a
comprising peptides and AAY91231-Y91235 comprise the immunogens comprising
antigen, and AAY91231 se and AAY91231-Y91232 comprise the immunogens comprising a
comprise and may be used in a malaria vaccine. AAY91288-Y91231 represent
comprised to prevent or treat
are HYV neutralising B-cell epitopes. AAY9128-Y91251 and
AAY91288-Y91273 are antigenic peptides comprising WYH Th and HYV-1 B-cell
comprised by thich may be used as a component in an anti-HIV-1 vaccine.
AAY91198 and AAY91199 are respectively an immunostimulatory invasin
contein epitope from Yersinia specias, and hinge spacer peptide, both of
contein epitope from Yersinia specias, and hinge spacer peptide,
comprised by the antigenic peptides, and hinge spacer peptide,
comprised by the antigenic peptides of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helper T cell epitope; peptide immunogen; LHRH;
luteinising hormone-releasing hormone; spermatogenesis; ovulation;
osetrus; sexual development; sex hormone; promiscuous T helper epitope;
vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
breast cancer; endometriosis; boar taint; meat quality; immunocastration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.7%; Score 64; DB 21; Length 25
48.0%; Pred. No. 0.0055;
iive 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide sequence of the invention.
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                            invention.
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                                                                                                      Synthetic helper T cell (Th) epitope and a target antigen, luteinising hormone-releasing hormone (LHRH). The peptide immunogens cause hormone-releasing hormone (LHRH). The peptide immunogens cause hormones pecific immune response to LHRH which is involved in regulation of specific immune response to LHRH which is involved in regulation of specific immunogenesis, own attain of a promiscuous T helper and secretion of sex hormones. Provision of a promiscuous T helper and secretion of sex hormones. Provision of a promiscuous T helper optimum immunogenity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast, also endometriosis); to prevent boar taint (and improve meat quality) and for immunocastration. The present sequence appears in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
epitope; prophylaxis; treatment; mimotope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
site and helper T cell epitope, for e.g. contraception and nt of cancer -
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                                                                                            specification describes peptide immunogens comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 21; Length 25;
Pred. No. 0.0055;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
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                                                        Disclosure; Page 92; 102pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                               45.7%;
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99US-0281760
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Best Local Similarity 48.0
Matches 12; Conservative
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                     treatment of
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30-MAR-1999;
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antigen
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AMY50876-Y50900 represent peptide mimotopes used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
can be used for prophylaxis or treatment of canine allergy. AAY50876-Y50900 represent peptide mimotopes used in the method of the
                                                                                                                                                                                                               Gaps
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                                                                                                                                                                Score 54; DB 21; Length 15;
Pred. No. 0.11;
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71.4%; Pred. No. 0.18;
ive 1; Mismatches 3;
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                                                                                                                                                           38.6%;
76.5%;
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| qcivdhpdf--pivrsi 15
                                                                                                                                                                                                            Conservative
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                                                                                                                                  Query Match
Best Local Similarity
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99EP-0107035
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Best Local Similarity
Matches 9; Conserv
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09-APR-1999;
                                  09-APR-1998;
30-MAR-1999;
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30-MAR-1999;
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                                                                                                                               Lawton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                               Peptide which binds to Immunoglobulin E (1gE) receptors inhibiting 1gE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
epitope; prophylaxis; treatment; mimotope.
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                                                                                                                                                                                                         Immunoglobulin E (IgE); anti-allergic drug; IgE binding inhibitor
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                                                                                                                                                                                                                                            Location/Qualifiers
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                                  AAR02179 standard; protein; 17
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/note="Ala-OH"
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Matches 9; Conserv
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Misc-difference
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                                                                       AAR02179;
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This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allargic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allargic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.

ANX50876-X50900 represent peptide mimotopes used in the method of the
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Pred. No. 14;
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); Mismatches
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                                                                                                                                               Francoeur G;
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ilarity 64.3%;
Conservative
98US-0058331
99US-0281760
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99US-0281760
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binds to native canine free or B-cell bound IgE, and which doesn't bind to 19g when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.

ANY50876-Y50900 represent peptide mimotopes used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.

ANYSOBY6-Y50900 represent peptide mimotopes used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
epitope; prophylaxis; treatment; mimotope.
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binding proteins used for treatment or prophylaxis of canine allergy
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                                                                                                                                                                                                                                  Length 17;
                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody 15A.2 feline IgE binding epitope 1.
                                                                                                                                                                                                                                                 ed. No. 14;
Mismatches
                                                                                                                                                                                                                                 Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Francoeur G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 7; 30pp; English.
                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                          AAY50897 standard; peptide; 17
                                                                                                                                                                                                                             Query Match 29.3%;
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99EP-0107035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0058331
99US-0281760
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                                                                                                                                                                                                                                                                                                                        (IDEX-) IDEXX LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mermer B,
                                                                                                                                                                                                                                                                                                    9 VDRPDFPKPIVRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-040833/04
                                                                                                                                                                          17 AA;
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30-MAR-1999;
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                                                                                                                                             nvention
                                                                                                                                                                            Sequence
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AAW24098-106 are peptide fragments containing at least 5 continuous maino acids of the partial canine immunoglobulin E (19E) protein shown in AAW24097. The peptides are used for the preparation of anti-canine IgE antibody. The anti-canine IgE antibody can be used for the diagnosis
                                                                                                                                                                                                                                                        Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canine immunoglobulin E peptide fragment and related DNA - useful for the preparation of anti-canine immunoglobulin E antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Podisus maculiventris; proline-rich; pathogenic; bacteria; bug;
Gram negative; plant treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proline-rich antibacterial peptide from Podisus maculiventris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.3%; Score 41; 64.3%; Pred. No. 1
                                                                                                                  AAW24102 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW09376 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 9; 12pp; Japanese.
                                                                                                                                                                                                                        Canine immunoglobin E peptide
                                                                                                                                                                                                                                                                                                                                                                                                 95JP-0334381
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22
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                Conservative
6 QSIVDRPDFPKPIVRSI
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA;
                                                                                                                                                                                                                                                                                          Canis familiaris.
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                                                                                                                                                                                                                                                                                                                           JP09169795-A.
                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1995;
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Gaps

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Length 17;

Score 41; DB 21; Pred. No. 14;

29.3%; 58.8%;

ed. No. 14; Mismatches

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Conservative

Query Match Best Local Similarity Matches 10; Conserv

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Gaps

5;

Query Match

27.5%; Score 38.5; DB 17; Length 16;
Best Local Similarity 43.8%; Pred. No. 31;
Matches 7; Conservative 4; Mismatches 0; Indels

9 VDRPDF----PKPIV 19
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oy ob Search completed: August 26, 2002, 10:18:42 Job time: 698 sec

Mon Aug- 26 11:09:36 2002

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Sequence 19, Appl
Sequence 54, Appl
Sequence 16, Appl
Sequence 72, Appl
Sequence 30, Appl
Sequence 120, Appl
Sequence 120, Appl
Sequence 180, Appl
Sequence 181, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 101, Appl
Sequence 103, Appl
Sequence 104, Appl
Sequence 105, Appl
Sequence 106, Appl
Sequence 107, Appl
Sequence 107, Appl
Sequence 107, Appl
Sequence 108, Appl
                                                                                                                      August 26, 2002, 10:19:37; Search time 33.13 Seconds (without alignments) 18.432 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgr2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgr2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgr2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgr2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgr2_6/ptodata/2/iaa/PorTuS_COMB.pep:*
/cgr2_6/ptodata/2/iaa/portuS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-447-010-14

US-08-447-411-19

US-08-642-227-16

US-08-107-947-16

US-08-107-947-10

US-08-107-947-10

US-08-107-947-30

US-08-107-947-30

US-08-107-947-120

US-08-107-947-120

US-08-107-947-120

US-08-107-947-120

US-08-107-947-15

US-08-107-947-15

US-08-107-947-15

US-08-447-11-58

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US-08-447-11-58

US-08-447-11-17

US-08-447-11-17

US-08-107-947-15

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US-08-107-947-15

US-08-107-947-15

US-08-107-947-15

US-08-107-947-15

US-08-107-947-19
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US-08-630-915A-165
US-08-466-975A-18
US-08-466-975A-19
                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                   231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                    1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
                                                                                                                                                                                                                                    US-09-701-623C-8
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l length: 0
| length: 25
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                                                                                                                                                                                                                                                                    perfect score:
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Maximum DB &
                                                                                                                 OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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                                                                                                                                                                               sequence 19, sequence 9, sequence 17, sequence 61, sequence 61, sequence 62, sequence 61, sequence 62, sequen
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US-08-391-671A-18
US-08-467-902A-19
US-08-467-902A-18
US-08-467-902A-19
US-09-275-265-18
US-09-275-265-19
US-09-122-1270-6
US-09-122-1270-6
US-08-146-028-61
US-08-146-028-62
US-08-146-028-122
US-08-123-425A-62
US-08-123-425A-122
US-08-723-425A-122
US-09-112-206-61
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Sequence 95, Application US/09100414B
Sequence 95, Application US/09100414B
Sequence 95, Application US/09100414B
Sequence 95, Application US/09100414B
SEQUENCEST WENTION: NOVEL LHRH PEPTIDE TITLE OF INVENTION: IMMUNOGENS TITLE OF INVENTION: IMMUNOGENS CORRESPONDENCE ADDRESS:
ADDRESSE: MOTGAN & Finnegan, L.L.P. ADDRESSE: MOTGAN & Finnegan, L.L.P. STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
COUNTRY: USA
ZIP: 10154-0054
ZIP: 10154-0054
ZIP: 10154-0054
ZIP: READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC Windows
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. Lin
REFERENCE/DOCKET NUMBER: 1151-4157
REFEREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGYGYQSIVDRPDFPKPIVRSITLC 25
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1 CGETYQSRVTHPHLPRALMRSTTKC 25
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MOLECULE TYPE: peptide
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US-09-100-414B-95
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APPLICANT: RRIZINGER, DAVID C.
APPLICANT: OF STIZINGER, DESCRIPTION OF SECURITY.
APPLICANT: VOGEL, CARL-WILHELM
TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 1; Length 16;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                           CLASSIFICATION 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/230,695
CLASSIFICATION NUMBER: US 07/888,132
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/888,132
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
REJETENTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1811-183 MIS:VG
TELEOMMUNICATION INFORMATION:
TELEPRA: 065-24567 SIMBAR
INFORMATION: TELEPA: 065-24567 SIMBAR
SEQUENCE CHARACTERISTICS:
TELEPA: 065-24567 SIMBAR
SEQUENCE CHARACTERISTICS:
TELEPA: 1153
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
TENTUM FOR SEQ ID NO: 14:
TELENT: 15 AND TO THE TELEPA: 165 AND TO THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.1%; Scc...
100.0%; Pred No. ...
... 0; Mismatches
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PRIOR APPLICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY, ARGENT INFORMATION:
NAME: Oblon, NO: 5773243man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-101-0
                                                                                              APPLICATION NUMBER: US/08/447,010
FILING DATE: 22-MAY-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/08447411; Patent No. 5773243; GENERAL INFORMATION:
                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.1
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide US-08-447-010-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 PDFPKP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111111
3 PDFPKP 8
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US-08-447-411-19
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Best Local Similarity 48.0%; Score 64; DB 4; Length 25;
Matches 12; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08447010
Patent No. 5770718
GENERAL INFORMATION:
APPLICANT MOFFATT, BARBARA
TITLE OF INVENTION: GENE FOR APRT FROM PLANT TISSUE
CORRESPONDENCE, 29
CORRESPONDENCE, ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Toronto
CONTRY: Canada
ZIP: MGG IR7
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PROPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
RESULT 2
US-09-303-323-95
Sequence 95, Application US/09303323
Sequence 95, Application US/09303323
Sequence 95, Application US/09303323
SEQUENCE INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTGAN & Finnegan, L.L.P.
STREET: 345 Park Avenue
STATE. NUMBER OF SECUENCES:
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, Suite 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
ELLING DATE: 30-APR-1999
RIOR APPLICATION STAR.:
APPLICATION NUMBER: US/09/303,323
FRICK APPLICATION NUMBER: 09/100,414
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29,323
REECOMMUNICATION INFORMATION:
RECISTRATION NUMBER: 29,323
REECOMMUNICATION INFORMATION:
TELEFOND 12-758-4809
THENERAL 212-758-4809
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGYGYQSIVDRPDFPKPIVRSITLC 25
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INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 25 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: Peptide US-09-303-323-95
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STREET: 300
TTY: TOTONTO
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                  Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 14-JUN-1996
CLASSIFICATION: 530
                Score 38; DB 1;
Pred. No. 16;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 2;
Pred. No. 16;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/09017947
Patent No. 6303754
GENERAL INFORMATION:
GAPLICANT: WOREL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: RECK, MICHAEL
APPLICANT: RETTZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: VOCEL, CARL-WILHELM
APPLICANT: REDEHORST, REINHORST
APPLICANT: ROCK, MICHAEL
APPLICANT: RTTZINCER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                           US-08-662-227-16; Sequence 16, Application US/08662227; Patent No. 5922320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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                27.18;
42.98;
Ouery Match
Best Local Similarity 42.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 21 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                              3 YGYQSIVDRPDFPK 16
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8 FGDDNIISRSDFPE 21
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8 FGDDNIISRSDFPE 21
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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Patent No. 5773243

GENERAL INFORMATION:
APPLICANT: FRITZINGER, DAVID C.
APPLICANT: BREDEHORST, REINHARD
APPLICANT: VOGEL, CARL-WILHELM
TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STRET: 1155 S. Jefferson Davis Highway, Suite 400
STATE: Virginia
                                                                                                                                                                                                                                                                                                        DB 1; Length 21; 16;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,411
                                                                                                                                                                                                                                                                                                        Score 38; DB 1
Pred. No. 16;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
            TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3300
TELEEX: (703) 413-2220
TELEX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                                          27.18;
42.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 248955 OPAT UR
INFORMATION FOR SEQ ID NO: 59
                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                      Query Match 27.1
Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                       MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
CRIGINAL SOURCE:
ORGANISM: Naja naja
US-08-447-411-59
                                                                                                                                                                                                                                                                                                                                                                                     3 YGYQSIVDRPDFPK 16
                                                                                                                                                                                                                                                                                                                                                                                                         : | : | : | ||:
8 FGDDNIISRSDFPE 21
                                                                                                                                                                                                                              ; ORGANISM: Naja naja
US-08-447-411-19
                                                                                                                                                                         linear
                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 22202
                                                                                                                                                                   TOPOLOGY:
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Gaps

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GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: RCCK, MIGHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 1; Length 22;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
FILING DATE: 14 -JUN-1996
CLASSIFICATION NUMBER: US/08/662,227
FILING DATE: 12 -JUN-1996
CLASSIFICATION NUMBER: 1126-0107-0X
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 577343man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-101-0
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 413-3000
TELEX: 248655 OPAT UR
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/08662227 Patent No. 5922320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.18;
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SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Naja naja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 YGYQSIVDRPDFPK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| :|: | |||:
8 FGDDNIISRSDFPE 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM:
US-08-447-411-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-662-227-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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Fatent No. 5773243
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PRIDEHORST, REINHARD
APPLICANT: VOGEL, CARL-WILHELM
TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 175 S. JEFFERSON DAVIS HIGHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 4; Length 21; Pred. No. 16;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
*APPLICATION NUMBER: US/08/447,411
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1126-0107-0X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/662,227
FILING DATE: 14-UN1-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-(TELECOMMUNICATION INCORMATION:
TELEPHONE: 703-413-3000
TELEFERAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                              COMPUTER: Floppy disk COMPUTER: IBM PC compatible ODERATING SYSTEM: PC-nnc AND SOFTWARD POPUTED AND PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 16:
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42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 42.9
Matches 6; Conservative
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                             ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-09-017-947-16
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8 FGDDNIISRSDFPE 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                     STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-447-411-72
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COUNTRY: U.S.A. ZIP: 10036-2711
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| PKPPIRSVSL 18
                                                                                                                                                                                                                                                        New York
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                                                                                                                                                                                                                                         New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                APPLICANT:
                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: WOGEL, CARL-WILHELM
APPLICANT: BREDEHORST; REINHORST
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STRRET: P.C.
STRRET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.1%; Score 38; DB 4; Length 22; 42.9%; Pred. No. 17;
                                                              Length 22,
                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/017,947 FILING DATE:
                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1126-0107-0X TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                               Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/662,227
FILING DATE: 14-UN-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-602-999A-120
; Sequence 120, Application US/08602999A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                      Sequence 30, Application US/09017947 Patent No. 6303754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: OBLON, NORMAN F. REGISTRATION NUMBER: 24,618
                                                            27.1%;
42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 amino acids
                                                                            Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                            3 YGYQSIVDRPDFPK 16
                                                                                                                                              3 YGYQSIVDRPDFPK 16
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8 FGDDNIISRSDFPE 21
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Best Local Similarity
6, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                     GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
; MOLECULE TYPE:
US-08-662-227-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
                                                                                                                                                                                                     RESULT 10
US-09-017-947-30
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                                                              Query Match
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APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFWAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian M.
APPLICANT: KCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
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               APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: DUR, Claurence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James B.
APPLICANT: RIDER, James B.
APPLICANT: RIDER, SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 20; 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/602,999A FILING DATE: 16-FEB-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB Pred. No. 31; 31; Mismatches
                                                                                                                                                                                                                                                               E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-630-915A-180
; Sequence 180, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Mistorock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 111
SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide US-08-602-999A-120
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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Gaps

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GENERAL INFORMATION:
APPLICANT: FRITZINGER, DAVID C.
APPLICANT: BREDEHORST, REINHARD
APPLICANT: OVGEL, CARL, WILHELM
TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                             NAME/KEY: Other
OTHER INFORMATION: May or may not have carboxy-terminal
OTHER INFORMATION: amide and/or biotinylated N-terminal
US-08-630-915A-222
                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 4; Length 20;
Pred. No. 31;
3; Mismatches 1: Indels
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STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/447,411
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
FILING DATE:
CLASSIFICATION NUMBER: 24,618
REFERENCE/COCKET NUMBER: 24,618
REFERENCE/COCKET NUMBER: 24,618
REFERENCE/COCKET NUMBER: 24,618
REFERENCE/COCKET NUMBER: 1126-101-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 58, Application US/08447411 Patent No. 5773243
                 TELEFAX: (212) 669-8867/9741
TELEX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 222:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                         25.7%;
60.0%;
(212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.v
                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                MOLECULE TYPE: peptide FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
                                                                                                                                                                                             linear
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9 PKPPIRSVSL 18
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  TELEPHONE:
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APPLICANT: HOFFWAN, No. 6309820h
APPLICANT: HOFFWAN, No. 6309820h
APPLICANT: KAY, BRIAN K.
APPLICANT: KAY, BRIAN K.
APPLICANT: KOWIKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: DOLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                 ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIDIA TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-630-915A-222
; Sequence 222, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION UNDBER: 1101-1
REFERENCE/DOCKET NUMBER: 1101-1
TELECOMMUNICATION INFORMATION:
TELERAX: (212) 790-9090
TELERAX: (212) 869-8864/9741
TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 180:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MISTOCK, S. Leslie
RECISTRATION NUMBER: 18,872
REEFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.7
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 PKPIVRSITL 24
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| PKPPIRSVSL 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-630-915A-180
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Sequence 15. Application US/0866227

Patent No. 592330

GENERAL INFORMATION

PAPLICANT: BREDEHORST, REINHORST

APPLICANT: BREDEHORST, REINHORST

APPLICANT: BREDEHORST, REINHORST

APPLICANT: RRITZINGER, DAVID

TITLE OF INVENTION: RECOMBINANT PROCVF

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: POBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, STREET: 1755 S. JEFFERSON DAVIS HIGHWAY

CITY: ARLINGTON NET PROPRY LISK

COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER FRADABLE FORM:
MEDIUM TYPE: 110 MAPPE: 0910

COMPUTER FRADABLE FORM:
MEDIUM TYPE: 110 MAPPE: 0910

SECHERAL OBLON, NORMAN F.

REFERENCE/DOCKET NUMBER: 1126-0107-0X

TELECOMMUNICATION INFORMATION:
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TREATMENT AND ACID A
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Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 2; Indels
       Score 35; DB 1; Length 21; Pred. No. 46;
                                                                               2; Indels
                                                                        1; Mismatches
       25.0%;
Query Match 25.0
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                             8 IVDRPDFPK 16
                                                                                                                                                                                  8 IVDRPDFPK 16
                                                                                                                                                                                                                                                                                                                 RESULT 15
US-08-662-227-15
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Search completed: August 26, 2002, 10:19:37 Job time: 393 sec

|: | |||| |13 IISRSDFPK 21

QQ

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 26, 2002, 10:20:42 ; Search time 43.94 Seconds (without alignments) 54.671 Million cell updates/sec

US-09-701-623C-84 Title: Perfect score:

135 1 CGETYKSTVSHPDLPREVVRSIAKC Sequence:

25

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

4981 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 25

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	serum albumin - do	superoxide dismuta				Ψ.	15K protein 5106 -	ribosomal protein	p7 protein - human	α	cytokeratin 4 - bo	hypothetical TEL/M	T-cell receptor be	superoxide dismuta	kinase-related tra	DNA (cytosine-5-)-		superoxide dismuta		chromogranin-B - r	T-cell receptor J-	seed protein ws-6	relaxin - baboon (nin	extension protein	metal-binding prot	prolylendopeptidas	outer layer protei	$\boldsymbol{\sigma}$
SUMMARIES							_			_																		_		
SU		29749	PS0186	530384	28027	3045	A61093	PS0251	S78765	S41390	A58647	146016	3335	9255	0012	1263	5641	н37196	0071	PH1822	D49164	7207	F61491	S42785	B37196	S48685	152	PC2280	3981	27
	ΩI	\$2	PS	83	12	ďΣ	A6.	PS	S7	S4	A5	14	13	A4	PA	A4	83	H3.	PA(PH	D40	S4.	F6.	S4.	B3,	S48	PL(Ω,	\$2.	A6]
	DB	7	~	7	7	N	~	7	~	7	7	~	4	~	N	7	7	7	7	~	7	~	~	7	~	~	~	7	7	7
	Query Match Length	24	19	16	23	25	20	15	11	23	25	6	15	16	19	23	24	10	15	17	20	21	23	24	10	14	14	18	20	20
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	Score	35	31	30	29	58	N	27.5	27	N	26.5	26	26	26	26	26	56	25	25	25	25	25	~	24.5	24	24	24	24	24	24
	Result No.	Т	7	m	₹	Ŋ	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote ribosomal protein	glandular kallikre alpha-conotoxin MI	superoxide dismuda T cell receptor al seed storage prote	protein OF200651 - T cell receptor al	110K protein - mou RNA-directed RNA p	major outer membra hypothetical prote	apolipoprotein E - nerve growth facto	probable acr-2 reg
S23637 JP0064	A54326 NTKN1M	S/4128 PH1806 PA0009	PA0088 PH1802	S18386 PQ0409	S28435 T01691	A05310 A56901	872535
23 2 25 2	13 2	14 2 2 15 2 2	15 2 17 2	18 2 19 2	70 70 70 70	20 21 2	23 2
17.8 17.8	17.0	17.0	17.0	17.0 17.0	17.0 17.0	17.0 17.0	17.0
24 24	233	233	233	23	23	23	23
30 31	33.2	3 3 4 3 5 4	37	39 40	41 42	43 44	45

ALIGNMENTS

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C;Species: Canis lupus familiaris (dog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: 529748
S;Dixon, J.W.; Sarkar, B.
J. Biol. Chem. 249, 5872-5877, 1974
A;Title: Isolabation, amino acid sequence and copper(II)-binding properties of peptide A;Title: Isolabation, amino acid sequence and copper(II)-binding properties of peptide A;Teference number: 529749; MUID:75011422
A;Reference number: 529749
A;Reference received by Muid: 75011422
A;Molecule type: protein
A;Molecule type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
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Pred. No. 1.2e+02;
3; Mismatches 8; Indels
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40.9%;
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Best Local Similarity 40.9
Matches 9; Conservative
serum albumin - dog
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3 ETYKSTVSH--PDLPREVVRSI 22 δ

1 EAYKSEIAHRYNDLGEEHFRGL 22 q

~ PS0186 RESULT

Four superoxide dismutase (EC 1.15.1.1) (Mn) - rice (fragment)
C;Species: Oryza sativa (rice)
R;Ramo, M.; Tsugita, A.
Submitted to JIPID, June 1991
A;Reference number: PSO184
A;Reference number: PSO186
A;Molecule type: protein
A;Residues: 1-19 < KAM>
A;Residues: 1-19 < KAM>
C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxyg C;Superfamily: superoxide dismutase (Mn) C;Keywords: manganese; metalloprotein; oxidoreductase

Gaps ; Length 19; 1; Indels Score 31; DB 2; I Pred. No. 3.7e+02; 1; Mismatches 1; 23.0%; 75.0%; Query Match 23.0 Best Local Similarity 75.0 Matches 6; Conservative

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8 TVSHPDLP 15 g ò

||: |||| 3 TVALPDLP 10

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Length 25,

530384

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C; Keywords: hydroxyproline; tandem repeat
F; 4, 14/Modified site: 3-hydroxyproline (Pro) #status experimental
F; 5, 9, 15, 19/Modified site: 4-hydroxyproline (Pro) #status experimental
F; 7, 11/Modified site: 3', 4'-dihydroxyphenylalanine (Tyr) #status experimental
F; 13/Modified site: 3', 4'-dihydroxyphenylalanine (Tyr) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the byssus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Comp. Physiol. B 156, 491-496, 1986
A;Title: Mussel glue from Mytilus californianus Conrad: a comparative study. A;Fitle: Mussel glue from Mytilus californianus Conrad: a comparative study. A;Feference number: A61093; MUID:86279063
A;Accession: A61093
A;Molecule type: protein
A;Residues: 1-20 <AMI>
A;Note: the amino terminal residue was tentatively identified as Ser
A;Note: 12-Ser was also found
C;Comment: This glue protein is a component of the adhesive plaque of the by
                                                                                                                                                                                                                                                                                                   glue protein - California mussel (fragments)
N:Alternate names: adhesive polyphenolic protein
C;Species: Mytilus californianus (California mussel)
C;Accession: A61093
R;Waite, J.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C;Accession: PS0251
B;Pederence number: PS0209
A;Reference number: PS0209
A;Accession: PS0251
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C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 2; Length 20;
Pred. No. 1.1e+03;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
Score 29; DB 2; Ler
Pred. No. 9.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15K protein 5106 - rice (strain Nihonbare) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27.5; DB 2;
Pred. No. 9.6e+02;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 1-15 < TSD.
Experimental source: germ, strain Nihonbare
C; Comment: molecular weight 15K, p1 9.2.
                        21.5%;
23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 20.7%;
Similarity 44.4%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.4%;
                                                                                                                                                            9 RSVIGRPETQRKTVEAL 25
                                                                                                                              6 KSTVSHPDLPREVVRSI 22
                                                                           Conservative
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                                             Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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6 TYKPKITYP 14
                           Query Match
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                                                                                                                                               C; Species: Pseudomonas putida
C; Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
C; Accession: S30384
R; Willey, D.L.; Caswell, D.A.; Lowe, C.R.; Bruce, N.C.
Biochem. J. 290, 539-544, 1993
A; Title: Nucleotide sequence and over-expression of morphine dehydrogenase, a plasmid-en
A; Reference number: S30383; MUID:93199531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Accession: 128027
R.Bauw, G.: De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A.Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-A.Accession: 128027
A.Accession: 128027
A.Accessions: 1-23 <ABAU>
C.Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R)ochi, K.
submitted to JIPID, February 1994
A)Bescribtion: Phylogenetic diversity in the genus Bacillus and comparative ribosomal A)Reference number: JP0042
A)Reference number: JP0045
A)Recession: JP0045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                              A;Accession: S30384
A;Status: preliminary; translation not shown
A;Molecule type: Dna
A;Residues: 1-16 cWIL>
A;Residues: 1-16 cWIL>
A;Cross-references: EMBL:M94775; NID:g1621506; PIDN:AAB17357.1; PID:g151367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         superoxide dismutase (EC 1.15.1.1) (Mn) - curled-leaved tobacco (fragment)
C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 05-Mar-1999
C;Accession: I28027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Staphylococcus aureus
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 03-May-1996
C;Accession: JP0045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 2; Length 16, pred. No. 4.4e+02; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribosomal protein L30 - Staphylococcus aureus (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Molecule type: protein
A.Residues: 1-25 <OCH>
C.Superfamily: Escherichia coli ribosomal protein L30
C.Keywordh; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29;
Pred. No.
                                                                                                                              hypothetical protein · Pseudomonas putida
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.2%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity
Matches 6; Conserv
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RESULT JP0045

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RESULT

128027

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C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C:Date: 21-Feb-1997 #text_cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: 146016
R; Blessing, M.; Jorcano, J.L.; Franke, W.W.
BMBO J. 8, 17-126, 1989
A; Title: Enhancer elements directing cell-type-specific expression of cytokeratin gen A; Reference number: 146016; MUID:89231609
A; Accession: 146016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A49555
T-cell receptor beta chain V-D-J-C region (V beta 7, J beta 1.6) - human (fragment)
C;Species: Homo sapiens (man)
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C;Comment: This sequence is the chimeric product of a translocation mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical TEL/MN1 mutant fusion protein type II - human (fragment)
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F;25/Modified site: amidated carboxyl end (Gln) #status experimental
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Pred. No. 2.8e+05;
1; Mismatches 0; Indels
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Pred. No. 2.3e+03;
2; Mismatches 4;
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83.3%;
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41.78;
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Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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C;Keywords: fusion protein
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A;Gene: ETV6/MN1; TEL/MN1
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 5; Conserv
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A. Residues: 1-25 < GRDP>
A. Reference number: A67666; PDB:LRPP
A. Reference number: A67666; PDB:LRPP
A. Reference number: A77666; PDB:LRPP
A. Reference number: A77 / 1997
B. Han, K.H.: Hwang, K.J.: KIM, S.M.: Kim, S.K.; Gray, W.R.; Olivera, B.M.; Rivier, J.; S. R. Han, K.H.: Hwang, K.J.: KIM, S.M.: Kim, S.K.; Gray, W.R.; Olivera, B.M.; Rivier, J.; S. A. Reference number: A568666; MUID:97200721
A. Title: NMR structure determination of a novel conotoxin, [Pro 7,13] alpha A-conotoxin A; Teference number: A56866; MUID:97200721
C. Superfamily: undassigned conotoxins
C. Superfamily: undassigned conotoxins
C. Superfamily: undassigned conotoxins at a midated carboxyl end; hydroxyproline; PDS
C. Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; PS; J.11,14-23/Disulfide bonds: #status experimental
F. 7,13/Modified site: 4-hydroxyproline (Pro) {partial} #status experimental
F. 70/Modified site: 4-hydroxyproline (Pro) *status experimental
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C;Species: Conus purpurascens (purple cone)
C;Species: Journal of the cone)
C;Date: 31-0ct-1997 #sequence_revision 07-Nov-1997 #text_change 15-Sep-2000
C;Accession: A58647
R;Hopkins, C.; Grilley, M.; Miller, C.; Shon, K.J.; Cruz, L.J.; Gray, W.R.; Dykert, J.; R;Hopkins, C.; Grilley, M.; Miller, C.; Shon, K.J.; Cruz, L.J.; Gray, W.R.; Dykert, J.; R;Hopkins, Chem. 270, 22316-22357, 1995
A;Title: A new family of Conus peptides targeted to the nicotinic acetylcholine receptor A;Reference number: A58647; MUID:95403432
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                                                                                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 1-11 <GRA>
C,Reywords: mitochondrion
F;1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental
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Pred. No. 1.8e+03;
1; Mismatches 6; Indels
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Pred. No. 8.2e+02;
5; Mismatches 2; Indels
                                                                                                                        R;Graack, H.R. submitted to the Protein Sequence Database, July 1999 A;Reference number: $78760 A;Accession: $78755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 20.0%;
Best Local Similarity 41.7%;
Matches 5; Conservative
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Search completed: August 26, 2002, 10:20:42 Job time: 348 sec
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C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C;Accession: A49255
R;Rosenberg, W, M.; Moss, P.A.; Bell, J.I.
Bur. J. Immunol. 22, 541-549; 1992
A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using A;Reference number: A49039; MUID:92164737
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Molecule type: squance extracted from NCBI backbone (NCBIP:90722)
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: PA0012
C;Accession: PA0012
Submitted to JIPID, July 1994
Submitted to JIPID, July 1994
A;Remo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
A;Bescription: Separation and characterization of Arabidopsis proteins by two-dimensiona A;Reference number: PA0012
A;Accession: PA0012
A;Accession: PA0012
A;Molecule type: protein
A;Residues: 1-19 <ARAM>A;Residues: allus
C;Superfamily: superroxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
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C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Accession: A41263
R; Lock, P; Ralph, S; Stanley, E; Boulet, I:; Ramsay, R;; Dunn, A.R.
A; Title: Two isoforms of murine hck, generated by utilization of alternative translation
A; Reference number: A41263
A; Reference number: A41263
A; Status: preliminary
A; Accession: A41263
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-23 < LOC>
C; Keywords: phosphotransferase
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Pred. No. 1.7e+03;
2; Mismatches 6; Indels
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Best Local Similarity 62.5%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels
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Best Local Similarity 31.2%; Pred. No. 2.5e+03;
Matches 5; Conservative 4; Mismatches 7; Indels
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Best Local Similarity 33.3%; Pre
Matches 4; Conservative 2;
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3 TFTLPDLP 10
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Best Local Similarity
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AC P81621;
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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CXA1_CONMA
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Match Length
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length: 25
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus thermophilus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
           couns
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                                                                                                            P82041
P82044
P28879
P80981
P80980
P81064
P46365
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P80501
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AC 02210;
DT 01-UNN-1994 (Rel. 29, Created)
DT 01-UNN-1994 (Rel. 29, Last sequence update)
DT 16-CCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in MORA 3'region (Fragment).
S Pseudomonas putida.
OG Plasmid pMDH7.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ore 32; DB 1;
ed. No. 78;
Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
CXA1_CONCN
LPH1_ECOLI
MMPX_SOLTU
UP34_UPEMJ
UP37_UPEMJ
CXA2_CONST

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Pred. No.
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MEDLINE=93199531; PubMed=8452544;
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66.78;
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CFPA_TREPH
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Physiol. 97:366-374(1991).
-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!- COFACTOR: Manganese (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                     Soba.
Hordeum vulgare (Barley).
Hordeum vulgare (Barley).
Eukaryota: Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: Mitochondrial matrix.
-i- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).
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C
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STRAIL CV. CM 72; TISSUE-ROOt;
Hurkman W.J., Tao H.P., Tanaka C.K.;
"Germin-like polypeptides increase in barley roots during salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                   Length 16;
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                                                                                                                                                                                                         3; Indels
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                                                                                                                                             16 AA; 1962 MW; A2F1EB8C172766ED CRC64;
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Pred. No. 1.2e+02;
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Mendel: 16446; HORvu;SodA;mn16446.
InterPro: IPR001189; SOD_MI.
Pfam: PF00081; sodfe: 1.
PROSITE: PS00088; SOD_MN; PARTIAL.
                                                                                           EMBL, M94775; AAB17357.1; -. PIR, S30384; S30384. Hypothetical protein; Plasmid. NON_TER 16 16
                                                                                                                                                                                22.2%;
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ATFTLPDLP 10
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P28524;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
PDB: 1P1P; 07-JUL-97.
Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                      Cruz L.J., Gray W.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "NMR structure determination of a novel conotoxin, [Pro 7,13] alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 36:1669-1677(1997).
-1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
INHIBIT THEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26.5; DB 1; Length 25;
                                                                                                                     Conus purpurascens (Purple cone).
Eukaryota, Metazoa, Mollusca, Gastropoda, Caenogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-KAZAN 5;
MEDLINE-96236033; Pubmed-8655496;
YOU Y., Elmore S., Colton L.L., Mackenzie C., Stoops J.K.,
Weinstock G.M., Norris S.J.;
                                                                                                                                                                                                                                                                                Hopkins C., Grilley M., Miller C., Shon K.-J., Cruz L.J., Dykert J., Rivier J., Yoshikami D., Olivera B.M.; An ew family of Conus peptides targeted to the nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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NCBI_TaxID-162;
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9E2147898D697640 CRC64;
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2; Mismatches 4
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cytoplasmic filament protein A (Fragment).
                                       01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Alpha-A conotoxin PIVA.
    25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYDROXYLATION.
HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYDROXYLATION
                                                                                                                                                                                                                                                                                                                                               acetylcholine receptor.";
J. Biol. Chem. 270:22361-22367(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydroxylation; Venom; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                 MEDLINE-95403432; PubMed-7673220;
                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR. MEDLINE-97200721; Pubmed-9048550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.6%;
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    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                  NCBI_TaxID=41690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A-conotoxin PIVA
                                                                                                                                                                                                                                            TISSUE-Venom;
CXA4_CONPU
P55963;
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P56738;
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MOD_RES
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SEQUENCE
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18.5%;
83.3%;
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Best Local Similarity 83...
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 5; Conserv
                                                                  NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 SHPDLP 15
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P80732:
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SEQUENCE
                                                                                                                  SEQUENCE
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SODN_STRGR
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*Characterization of the cytoplasmic filament protein gene (cfpA) of Treponema pallidum subsp. pallidum.";
J. Bacteriol. 178:3177-3187(1996).
-! FUNCTION: COMPONENT OF THE CYTOPLASMIC FILAMENTS THAT RUN THE LENGTH OF THE ORGANISM JUST UNDERMEATH THE CYTOPLASMIC MEMBRANE.
-!- SUBCELLULAR LOCATION: AN ARRAY OF 4 TO 6 FILAMENTS LIE IN CLOSE APPOSITION TO THE INNER MEMBRANE AND ARE ALMAYS LOCALIZED DIRECTLY UNDERNEATH THE CORRESPONDING GROUP OF PERIPLASMIC FLAGELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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01-007-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bothrops insularis (Island jararaca) (Queimada jararaca). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
                                                                                                                                                                                                                                                                                                                       Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.5%; Score 25; DB 1; Length 10; 60.0%; Pred. No. 4.2e+02; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  Score 26; DB 1; Length 21;
Pred. No. 6.8e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                  21 AA; 2231 MW; 574604B4FFC2D017 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 AA.
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                                                                                                                                                                                                                                                                                                                  19.3%;
50.0%;
                                                                                                                                                                                                     Structural protein; Antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AA; 1173 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypotensive agent; Venom.
                                                                                                                                                                                                                                                                                                                Query Match 19.3
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOD2.
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              11 VFHPEKPSAV 20
                                                                                                                                                                                                                                                                                                                                                                                                          9 VSHPDLPREV 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme inhibitor).
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|HPNIP 9
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P54712;
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SEQUENCE
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-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
                                                                                                                                                                                                                                                                                                                                                                        --- COFACTOR: Manganese (By Similarity).
--- SUBUNT: HOWOTERRAMEN (BY SIMILARITY).
--- SUBUNT: HOWOTERRAMEN (BY SIMILARITY).
--- SUBUSELLULAR LOCATION: MITCOCHONDINAL matrix.
--- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Supercxide dismutase [Ni] (EC 1.15.1.1) (NiSOD) (Nickel-containing superoxide dismutase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBI_TaxID=1911;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó;
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MEDLINE=97056064; PubMed=8900409;
Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Hah Y.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces griseus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER 13 13 A76 MW; 9C9651DE8BE0672A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 1; I
Pred. No. 5.6e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; Manganese; Mitochondrion.
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-i- SUBCELLULAR LOCATION: Cytoplasmic.
Oxidoreductase; Nickel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P04179; 1AP6.
HSC-2DPAGE; P54712; DOG.
HTGFPPO; PR001189; SOD_MI.
Pfam; PF00081; sodfe; 1.
PROSITE; PS00088; SOD_MN; PARTIAL.
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6 KSTVSHPD-LPRE 17
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Best Local Similarity
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Best Local Similarity
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1 KTGVNKPELLPKE
                                                                                                                                                                                                                      20 AA;
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PELPR 20
                         TISSUE-Needle;
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ID TL14_SPIOL
                                                                                        proteins.
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                  P82682;
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                                                                                                                                                                                                                                                                                                                        coli.";
Eur. J. Blochem. 207:839-846(1992).
-1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of needles (N147) (Fragments).
Pinus pinaster (Maritime pine).
Radayyopa, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinascae; Pinus.
NCBI_Tax_ID=71647;
                                                                                                                                                                                                                                                                                             "Sequence of the tufA gene encoding elongation factor EF-Tu from Thermus aquaticus and overproduction of the protein in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                        loss R.H., Hartmann R.K., Lippmann C., Alexander C., Jahn O.,
                                                                                                                                                                                             Thermus/Deinococcus group; Thermus group; Thermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.5%; Score 25; DB 1; Length 17; 21.4%; Pred. No. 7.6e+02; Live 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X66322; CAA46997.1; -.
PIR; S29294; S29294.
HSSP; P13551; 1DAR.
InterPro; IPR000795; GTP_EFTU.
PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
Elongation factor; Protein biosynthesis; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 17 AA; 2094 MW; EA46E1EF05F86E1D CRC64;
                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Elongation factor G (EF-G) (Fragment).
Thermus aquaticus.
                                                                                       17 AA.
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                                                                                        PRT;
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                                                                                                                                                                                                                                             STRAIN-EP 00276;
MEDLINE-92362620; Pubmed-1499561;
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                                                                                                                                                                                                                                                                                                                                                                                                                 EF-G/EF-2 SUBFAMILY.
                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
HPDLPREV 18
                                                                                                                                                                                                          NCBI_TaxID=271;
                        1 HSDLPSGV
                                                                                                                                                                                                                                                                                     Erdmann V.;
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ID UNOS_PINPS
AC P81674;
                                                                                     EFG_THEAQ
Q01697;
                                                                                                                                                                                              Bacteria;
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11
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
enzyme inhibitor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
17 ylakoid lumenal 14.7 kpa protein (P14.7) (Fragment).
Spinacia oleracea (Spinach).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TAXID=3562;
                  Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plomion C.; "Separation and characterization of needle and xylem maritime pine
                                                                                                                        Electrophoresis 20:1098-1108(1999).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.6, ITS MW IS: 36 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kieselbach T., Pettersson U., Bystedt M., Schroeder W.P.;
Submitted (JUL-2000) to the SWISS-PROT data bank.
-!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Botírops insularís (Island Jararaca) (Queimada Jararaca).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 1; Length 20;
Pred. No. 9.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                        9F4E4678E086C298 CRC64;
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MEDLINE-99274088; PubMed-10344291;
                                                                                                                                                                                                                                                                                                                                                                                                                               18.5%;
80.0%;
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Abe Y., Okazaki T.; "Purification and properties of the manganese superoxide dismutase from the liver of bullfrog, Rana catesbelana."; Arch. Biochem. Biophys. 253:241-248(1987).
-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Vitelline membrane outer layer protein II (VMO-II) (VMOII) (Fragment)
                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kido S., Morimoto A., Kim F., Doi Y.;
"Isolation of a novel protein from the outer layer of the vitelline membrane.";
Biochem. J. 286:17-22(1992).
-!- FUNCTION. EXACT FUNCTION NOT KNOWN, COMPONENT OF THE OUTER MEMBRANE OF THE VITELLINE LAYER OF THE EGG.
-!- PTM: ALL CYSTEINE RESIDUES OF THE MATURE PROTEIN ARE INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).
Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).
Ena catesbelana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphiblia; Batrachia; Annra; Neobatrachia; Ranoidea; Rana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 1; Length 20;
Pred. No. 1.3e+03;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 AA; 2325 MW; 45FC7989AB7527C7 CRC64;
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                                                                  20 AA
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                                                               PRT;
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InterPro; 1PR001189; SOD_MI.
Pfam: PF00081; sodfe; 1.
PROSITE; PS00088; SOD_MN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Egg Yolk;
MEDLINE=92392273; PubMed=1520265;
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MEDLINE=87126854; PubMed=3492965;
   RESULT 14

VMO2_CHICK STANDARD; F

AC Q9P549;

DT 16-OCT-2001 (Rel. 40, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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SEQUENCE
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SODM_RANCA
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                                                                                                            TISSUE-Venom;
MEDLINE-9031557; PubMed-2386615;
Cintra A.C.O., Vieira C.A., Giglio J.R.;
Cintra A.C.O., Vieira C.A., Giglio J.R.;
Frimary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
J. Protein Chem. 9:221-227(1990)
-!-FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININ BY INDIRECT HYPOTENSIVE AGENT.
IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
PIR: B37196; B37196
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
aurein 2.4 (Contains: Aurein 2.4.1].
Litoria aurea (Green and golden bell frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Granular dorsal gland;

BDLINE-20408845; Pubmed=10951191;

Rozek T., Regener K.L., Bowie J.H., Olver I.N., Carver J.A.,

Wallace J.C., Tyler M.J.;

Wallace J.C., Tyler M.J.;

Wallace J.C., Tyler m.J.;

Wallace J.C., Tyler m.J.;

Buthalian bell frogs Litoria aurea and Litoria raniformis the solution structure of aurein 1.2.";

Eur. J. Blochem. 267:5330-5341(2000).

I. FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,

L.INNOCUA, M.LUTEUS, S. AUREUS, S. EPIDERMIDIS AND S.UBERIS.

PROBABLY ACTS BY DISTURBING MEMBRARE FUNCTIONS WITH ITS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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AUREIN 2.4.1.
AMIDATION. '
1D87980438AAE2F9 CRC64;
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Pred. No. 1e+03;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24; DB 1;
Pred. No. 6e+02;
1; Mismatches
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      Crotalinae; Bothrops
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4 DIVKKVVGTIA 14
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 5; Conserv
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                                    NCBI_TaxID=8723
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5 HPQIP 9
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P82391;
Viperidae;
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SEQUENCE
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Query Match	17.8%;	17.8%; Score 24; DB 1; Leng
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Search completed: August 26, 2002, 10:30:18 Job time: 638 sec

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09171 Frochloroco
09x3d5 prochloroco
09x3d8 prochloroco
09x3d8 prochloroco
09591 staphylococo
028069 bos taurus
095713 prochloroco
095713 prochloroco
09567 revirus (t
09wv2 prochloroco
08567 revirus (t
05291 human adeno
05x3c2 prochloroco
028093 bos taurus
0913m8 rattus norv
093x3d14 prochloroco
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013659 homo sapien
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"Identification of cysteine-319 as the target amino acid of 8-[(4-bromo-2,3-dioxobuty1)thio]adenosine 5'-triphosphate in bovine liver glutamate dehydrogenase.";
Blochemistry 30:1126-7134(1991).
SEQUENCE 24 AA; 2669 MW; D67A84AE4264E740 CRC64;
                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
6LUTAMATE DEHYDROGENASE [EC 1.4.1.3) (FRAGMENT).
Bos taurus (Bovine).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos.
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Q9X3M3
Q9U8M9
Q9PRS2
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Best Local Similarity 50.0
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O9t2q0 solanum tub
O94118 oryza sativ
O67964 prochloroco
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                                                         August 26, 2002, 10:29:35; Search time 62.22 Seconds
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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1 CGETYKSTVSHPDLPREVVRSIAKC 25
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Listing first 45 summaries
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SEQUENCE FROM N.A.

MEDLINE=95242701; PubMed=7725672;

MCOILSTAIN A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;

Koffer A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;

Characterization of mutants of the vitemin-D-binding protein/group

Specific component: GC aborigine (1A1) from Australian aborigines and

South African blacks, and 2A9 from south Germany.";

Vox Sang. 68:50-54(1995).

ENBL: S77130; AAD14250.1; -.

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17

SEQUENCE 17 AA; 1845 MW; BB26CAD60293722C CRC64;
               MEDLINE-97444372; PubMed-9298993;
McNagny K.M., Pettersson I., Rossi F., Flamme I., Shevchenko A.,
Mann M., Graf T.;
"Thrombomucin, a novel cell surface protein that defines thrombocytes
and multipotent hematopoietic progenitors.";
J. Cell Biol. 138:1395-1407(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
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Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
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4.2e+02;
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Urbach E., Chisholm S.W.;
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Best Local Similarity
Matches 6; Conserv
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Urbach E., Chisholm S.W.;
Urbach E., Chisholm S.W.;
Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";
Limnol. Oceanog. 43:1615-1630(1998).
EMBL: AF070129; AAD20735.1;
NON_TER
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Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archgeauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus,
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Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95007849; Pubmed-7923441;
Miller M.J., Parmelee D.C., Benjamin T., Sechi S., Dooley K.L.,
Kadlubar F.F.;
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                                            Prochlorococcus sp.
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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Pred. No. 3.7e+02;
2; Mismatches 2; Indels
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Pred. No. 3.3e+02;
2; Mismatches 6; Indels
                                                                                                                                                                                                                       SEQUENCE 21 AA; 2318 MW; 78824B529A2C9262 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chem.-Biol. Interact. 93:221-234(1994).
SEQUENCE 17 AA; 2024 MW; 1D39F70F7D23B269 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update) CYTOCHROME B6/F COMPLEX SUBUNIT IV (FRAGMENT).
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01-JAN-1998 (TEMBLEEL: 05, La
01-DEC-2001 (TEMBLEEL: 19, La
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NCBI_TaxID=1220;
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"Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream."; Limnol. Oceanog. 43:1615-1630(1998).
EMBL; AF070190; AAD23280.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia, Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91139577; pubMed-199588;
yoo T., Bourne J.C., Blumenthal R.M.;
"A family of regulatory genes associated with type II restriction-modification systems.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEMARTING G.N., Proske R.J., Moomaw C.R., Strong A.A., Song X., Hisamatsu H., Tanaka K., Slaughter C.A.; "Identification, purification, and characterization of a PA700-dependent activator of the proteasome."; J. Blol. Chem. 271:3112-3118(1996).

SEQUENCE 16 AA; 1888 MW; FFBA93148F3A7BF4 CRC64;
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                                                                                                                                                                                                                          Length 21;
                                                                                                                                                                                                                                                               Indels
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BMBL; M63621; AAA24560.1; -.
NON.TER
SEQUENCE 11 AA: 1296 MW; 3039A71A34472AB7 CRC64;
                                                                                                                                                                CC946FFCC02C854F CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
PA700 SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30, Pred. No. 4.7e+02;
                                                                                                                                                                                                                        Score 30.5; DB 2;
Pred. No. 7.8e+02;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.2%; Score 30; DB 2; 83.3%; Pred. No. 4.7e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                11 AA.
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                                                                                                                                                              21 AA; 2298 MW;
                                                                                                                                                                                                                      Query Match 22.6%;
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, REASE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                          1: || :|| 3 STLKKPDLADPKLRSKLAK 20
                                                                                                                                                                                                                                                                                                     7 STVSHPDLPREVVRS-IAK 24
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Best Local Similarity 83.3
Matches 5; Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
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1 MSHPDL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations of two proteins in the retina."; Exp. Eye Res. 62:211-219(1996). SEQUENCE 20 AA; 2411 MW; 5F1A6AEB5918F777 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-JUN-2000 (TERBLEL] 14, Last annotation update)
ALBUMIN (FRAGMENT).
ALBUMIN (FRAGMENT).
Bukacas fassicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                      Ishikawa F., Matunis M.J., Dreyfuss G., Cech T.R.;
"Nuclear proteins that bind the pre-mRNA 3' splice site sequence (TUGAG/G) and the human telomeric DNA sequence d(TTAGGG)n.";
Mol. Cell. Biol. 13:4301-4310(1993).
SEQUENCE 20 AA: 2255 MW; C3CE1955E9A6D210 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicolas M.G., Fujiki K., Murayama K., Suzuki M.T., Mineki R.,
Hayakawa M., Yoshikawa Y., Cho F., Kanai A.;
"Studies on the mechanism of early onset macular degeneration in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.2%; Score 30; DB 6; Length 20; 55.6%; Pred. No. 8.9e+02; ive 3; Mismatches 1; Indels
                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
D(TTAGGG)N-BINDING PROTEIN B39 (FRAGMENT).
20 AA
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PRT;
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MEDLINE-93309464; PubMed-8321232;
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Biochem. Mol. Biol. Int. 36:67-75(1995).

-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).

-!- CATALYIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = 0(2) + H(2)0(2).

-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fester T., Schuster W.;
"Potato mitochondrial manganese superoxide dismutase is an RNA-binding
protein.";
                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                     SEQUENCE.
SEQUENCE.
SEQUENCE.
SEQUENCE.
OZLURK D.H., Colman R.F.;
"Identification of cysteine-319 as the target amino acid of 8-[(4-bromo-2,3-dioxobuty1)thio]adenosine 5'-triphosphate in bovine liver glutamate dehydrogenase.";
SEQUENCE 24 AA; 2626 MW; DE4ED4B54264E740 CRC64;
                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Peprantophyta; Peprantophyta; Peprantophyta; Spermatophyta; Core endicots; Asteridae; enasterida I; Solanales; Solanaceae; Solanum. NCBI_TaxID=4113;
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                                                                                                                                                                                                                                                                                                               4; Indels
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SEQUENCE 25 AA; 2713 MW; 45E0DA2EB3ADBCB3 CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (FRAGMENT).
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Last annotation update)
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75.0%; Pred. No. 1.6e+03;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                               Score 29; DB 6; 1
Pred. No. 1.5e+03;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                               25 AA.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotati
MANGANESE SUPEROXIDE DISMUTASE (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95392474; PubMed=7545053;
                                                                                                                                                                                                                                                                                21.5%;
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ProDom; PD000475; SOD_MI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuberosum (Potato).
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Best Local Similarity 41.7
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                    Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                  Wu S., de Lencastre H., Tomasz A.;
"Sigma-B, a putative operon encoding alternate sigma factor of
Staphylococcus aureus RNA polymerase: molecular cloning and DNA
sequencing.";
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae.
NCBL_TaxID=286;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30; DB 2; Length 23;
Pred. No. 1e+03;
1; Mismatches 3; Indels
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Pred. No. 9.9e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                      23 AA; 2541 MW; 7F47717B1767D34F CRC64;
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                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                             Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=1280;
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                                                                                                       Created)
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01-MAY-2000 (TrEMBLrel. 13, Created)
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EMBL; Y09929; CAA71063.1; -.
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MEDLINE-96427339; PubMed-8830703;
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                                                                                                     01-MAY-1997 (TrEMBLrel. 03,
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Best Local Similarity 60.0
احد 6; Conservative
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Matches 5; Conservative
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MEDLINB-21482706; PubMed-11598238;
Lee Y., Kende H.;
"Expression of beta-Expansins is Correlated with Internodal Elongation in Deepwater Rice.";
Plant Physiol. 127:645-654(2001).
EMBL: AX046927; AAL04420.1; -.
NON_TER 1
SEQUENCE 24 AA; 2649 MW; 16033EB00FDAEI2B CRC64;
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                                                                                                     Oryza sativa (Rice).
Bukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EXPB11.
       24 AA.
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       PRT;
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Antibody 15A.2 swi Antibody 15A.2 bin Antibody 15A.2 can Antibody 15A.2 gre Antibody 15A.2 gre Antibody 15A.2 bum 1gE derived target Human 1gE C epsilo Peptide #13 having Peptide #3 having Human 1gE C epsilo Peptide #4 having Human 1gE C epsilo Peptide #3 having Human 1gE C epsilo Peptide #7X derive 1gE peptide #11.

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ALIGNMENTS
           AAY50893
AAY50894
AAY50896
AAY50896
AAX50895
AAX50896
AAX5089
AAX10689
AAX72687
AAX106830
AAX10833
AAX1633
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AAM76742
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  15-MAY-2000 (first entry)
 AAY80077;
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A_Geneseq_032802:*

| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                              747574 seqs, 111073796 residues
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1 CGETYKSTVSHPDLPREVVRSIAKC
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Scoring table:

Searched:

Human bone marrow
Peptide #10886 enc
Dog allergen serum
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Human immunoglobul Cow milk alpha S1 Cow milk alpha S1

HSV-2 glycoprotein Peptide #10525 enc Human brain expres

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. the 18 . 9

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epitope; antigenic peptide from the CH3 domain of immunoglobulin E, fusions immunization against allergy $\,$ Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epit antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis. Optimised IgE-CH3 domain antigen peptide for horse IgE. (UNBI-) UNITED BIOMEDICAL INC. 98US-0100287. 99WO-US13959 Wang CY, Walfield AM; WPI; 2000-160578/14. Equus caballus WO9967293-A1 21-JUN-1999; 20-JUN-1998; 29-DEC-1999 Synthetic New

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sapiens.
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                                          antiganic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-archmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of 1gE, and so preventing triggering and activation of mast cells and basophils and downregulation of 1gE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against 1gE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAX80084 represent amino conformation.
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                                    The present invention describes immunoglobulin E (IgE)-CH3 domain
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100.0%; Pred. No. 1.9e-14;
iive 0; Mismatches 0;
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specific for a target effector site on the epsilon-heavy chain of 1gE, and so preventing triggering and activation of mast cells and basophils and downregulation of 1gE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against 1gE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermattis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiseuous T helper cell epitope (I) that include a promiseuous T helper cell epitope conjugates of (I) that include a promiseuous T helper cell epitope (I) that include a promiseuous T helper cell epitope constraints (disuffide bridge) to stabilise conformational features and maninace cross reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY7994 to AAY80084 represent mino acid sequences used in the exemplification of the present invention.
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Pred. No. 1.1e-09;
4; Mismatches 3;
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72.0%;
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Best Local Similarity 72.0°
Matches 18; Conservative
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The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesteryl ester transport protein (CETP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malania); for cancer immunotherapy; for inhibition of the action of luteinising hormone celesasing hormone (LHRH) for contraception, treatment of hormone-
refombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAN79994 to AAN80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; lutefulsing hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic; Plasmodium falciparum; circumsporozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis
                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                          69.6%; Score 94; DB 21; Length 25; 64.0%; Pred. No. 6.1e-08;
                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified human 1gE CH3 domain, SEQ ID NO:92.
                                                                                                                                                                                                                                                                                 4; Mismatches
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                                                                                                                                                                                                                                                                                                                    1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                           or human immune deficiency virus
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                25 AA;
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dependent cancer, prevention of boar taint in meat, and concording to promoting the growth of animals; or for inmunocastration; for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous or treating allergies or arteriosclerosis. Incorporation of a promiscuous or improves capacity to induce a strong Thelper cell-mediated immune response, resulting in production of antibodies against a target antigion. The arreplace carrier proteins and pathopach derived Thelper epitopes. Sequence AAY91121 represents a promiscuous Thelper epitope from the measles virus F (MYV) protein and sequences AAY91122. 1913.6.

WAY9126 and AAY9125 are present synthetic The pitope based on the heatilist B virus (HWY) surface antigen, and sequences AAY9114. Paper epitope AAY91157 are synthetic epitopes derived from this HBV epitope. AAY91157 are synthetic epitopes derived from this HBV epitope. AAY91157 and AAY91207 and AAY91204 virus of AAY91156-Y91306. AAY91207 and AAY91204 virus of AAY91166-AAY91166. AAY91167-Y91306 as comprising an LHRH sequence joined to a promiscuous Thepitope. AAY91197 peptides comprising somatostatin and AAY91201-Y91207 are artigenic peptides comprising somatostatin and Thepitope. Somatostatin for peptides comprising somatostatin and Thepitope. Somatostatin and human CO4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH The infection of T cells. AAY90212 sequence growth in livestock. AAY91208 is a peptide which may be used to promote growth in any be used to promote growth in the growth of T cells. AAY90212 is a modified version of a human IgE (immunoglobulin E) Tolls domain, and AAY90213-Y90219 are Thepitope. AAY91201 is a peptide end and AAY91221 is a modified version of a human ige controled by the derived from foot and mouth disease virus (FWDV) by the peptide and AAY91223 is a phasmodium falciparum circumsporozoite (CS) artigen on and AAY91223 is a phasmodium falcipar medical and AAY91232 are antigenic peptides and AAY91223 or antigen and and and
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antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies and anti-asthmatic properties. (I) induces polyclonal antibodies of specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. (compinant production of corresponding peptides or in DNA vaccines. (inctional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino caid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobulin immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-acthmatic; asthma; anaphylaxis; dermatitis.
                                               New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
                                                                                                                                     The present invention describes immunoglobulin E (IgE)-CH3 domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Optimised IgE-CH3 domain antigen peptide for mouse IgE.
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               WPI; 2000-160578/14.
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les 15; Conser
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Synthetic.
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                                                                                                                                                                                                                                                                                 The specification describes peptide immunogens comprising a synthetic helper T cell (Th) epitope and a target antigen, luteinising hormone-releasing hormone (LHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, oestrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast, also endometriosis); to prevent boar taint (and improve meat quality) and for immunocastration. The present sequence appears in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; fimmunoglobulin immunostimulatory; carrier protein; helper T cell epitope; antibody; allergic disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                  New peptide immunogen containing luteinising hormone-releasing hormone antigen site and helper T cell epitope, for e.g. contraception and treatment of cancer
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-has 5; Indels
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                                                                                (UNBI-) UNITED BIOMEDICAL INC
               99WO-US13960.
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     Query Match
Best Local Simmatches 11;
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                              The present invention describes immunoglobulin E (IgE)-CH3 domain antibodies antigent peptides (I). (I) have anti-allergic, anti-anaphylactic antigent peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AA779994 to AAX80084 represent amino
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Pred. No. 9.3e-05;
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Claim 1; Page 100; 155pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine immunoglobin E peptide 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 9; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW24102 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                       54.8%;
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Best Local Similarity 52.0
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                  25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 AA;
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                                                                                                                                                                                                                                                                                                                                                                  Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.

ANY50876-Y50900 represent peptide mimotopes used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding proteins used for treatment or prophylaxis of canine allergy
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  Score 63; DB 18; Length 20;
Pred. No. 0.004;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Antibody 15A.2 equine IgE binding epitope 1.
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                                                                                                                                                                                                                                                          AAY50900 standard; peptide; 16 AA.
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46.78;
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Matches 11; Conservative
                                                   Conservative
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4 vthphlpkdivrsiak 19
                                                                                               VSHPDLPREVVRSIAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KSTVSHPDLPRE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-040833/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY42585;
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WPI; 2000-040833/04
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                    21-APR-1994;
                                       14-AUG-1991;
                                                  07-JAN-1994;
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12-0CT-1999
                                                                                         Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                 diseases
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
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Matches
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                                                                                                                                                                                                                                                                                                                The invention provides immunoglobulin E (IgE) antagonists comprising one or more of the FcepsilonRI receptor-binding determinant sites of human IgE. The antagonists include IgE variants comprising an immunoglobulin template and binding determinant sequences (bds) CDbds, EFbds and the sequence shown in AAY4281. The CDbds (CD loop binding determinant the EFbds (EF loop binding determinant sequence) are selected from the sequences shown in AAY42578 and the EFbds (EF loop binding determinant sequences are selected from sequences shown in AAY42578 442580. The variants are useful in raising and screening anti-IgE antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment and prophylaxis of allergic
                                                                                                                                                                                                                                             Immunoglobulin E variants as peptide antagonists useful for raising and screening anti-immunoglobulin E (IGE) antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                             IgE; antagonist; FcepsilonRI receptor; human; bds;
binding determinant sequence; anti-IgE antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;
receptor-binding; binding determinant sequence; anti-IgE antibody;
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Pred. No. 0.028;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.0%;
                                                                                                                                94US-0232539
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getyqcrvthphlpralm 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 43.0
Best Local Similarity 55.6
Matches 10; Conservative
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                                                                                                                                                                                                       Jardieu PM, Presta LG;
         IgE peptide antagonist
                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                         WPI; 1999-579941/49.
                           Immunoglobulin E; receptor-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                allergic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allergic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                 21-APR-1994;
                                                                      Homo sapiens
                                                                                                                                                     14-AUG-1991;
                                                                                                                                                               07-JAN-1994;
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                                                                                         US5965709-A
                                                                                                             12-OCT-1999
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                                                                                                                                                                                                                                                                             diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                        diseases
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                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin E variants as peptide antagonists useful for raising and screening anti-immunoglobulin E (IgE) antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY50898 standard; peptide; 17
94US-0232539
                                                            91US-0744768.
94US-0178583.
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7 getyqcrvthphlpralm 24
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                                                                                                                                                                                                                            Presta LG;
                                                                                                                                                         (GETH ) GENENTECH INC.
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les 10; Conser
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Gaps

AA;

17

Sequence

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Binding proteins used for treatment or prophylaxis of canine allergy
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                Disclosure; Fig 7; 30pp; English
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                                                                                                          40.78;
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99US-0281760.
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                                                                                                                                                                                                (first entry)
                                                                                                                      Conservative
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4 vthpdlpkpilrsi 17
                                                                                                                                                                                                                                                                                                     (IDEX-) IDEXX LAB INC.
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                                                                                                   Query Match
Best Local Similarity
9, Conserv?
                                                                                                                                 9 VSHPDLPREVVRSI
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                                                                                                                                                                                                                                                              17-NOV-1999
                                                                               invention.
                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                                    AAY50893;
                                                                                         Sequence
                                                                                                                                                              RESULT 13
                                                                                                                                                                   AAY50893
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This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.

ANYSOB;6-Y50900 represent peptide mimotopes used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                        Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
epitope; prophylaxis; treatment; mimotope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Binding proteins used for treatment or prophylaxis of canine allergy
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Score 54; DB 21; Length 17;
Pred. No. 0.088;
4; Mismatches 1; Indels
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Pred. No. 0.088;
                                                                                                                                                                                                                                                                                                                                                    Antibody 15A.2 canine IgE binding epitope 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                           AAY50894 standard; peptide; 17 AA.
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      40.0%;
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Best Local Similarity 64.3.
9; Conservative
                       Similarity 64.3
9; Conservative
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4 vthphlpkdivrsi 17
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                                 This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound igE, and which doesn't bind to igE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound igE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.

ANYSOB/6-YSO900 represent peptide mimotopes used in the method of the
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epitope; prophylaxis; treatment; mimotope.
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                                                                                  Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
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                                                        Antibody 15A.2 feline IgE binding epitope 1.
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30-MAR-1999;
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                                                                                                                               Synthetic.
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AAY50897;
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Search completed: August 26, 2002, 10:18:43 Job time: 699 sec

4 vthpdlplvivrsi 17

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August 26, 2002, 10:29:34 ; Search time 62.22 Seconds (without alignments) 69:509 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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141
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

sp_plant:*
sp_rodent:*

Database :

Description	Q16310 homo sapien Q953a2 sus scrofa Q90rh8 human immun Q912r0 colanum tub Q90r14 mus sp. pro P5839 staphylococ Q90w14 mus sp. pro P95839 staphylococ Q90w15 dalus gall Q9uem3 homo sapien Q13665 homo sapien Q9xsq1 bos tarrus Q9bqt0 homo sapien Q8x667 recvirus (t Q9zej4 anabaena sp P90342 saccharomyc Q90403 discopyge o Q918k0 enterococcu
SUMMARIES	Q16310 Q95JA2 Q90RHB Q97RR0 Q90WA2 Q90WA2 Q90WA2 Q90EM3 Q13665 Q98EM3 Q98EG7 Q98EM3 Q98EM3 Q98EM3 Q98EM3 Q98EM3 Q98EM3 Q98EM3 Q98EM3
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18 AA.

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09TR98 016271 042416 090RH4 09UBN2 09UBN2 091CL6 091CC6 091C60 095895 091C60 0958387 091C80 0958387 090KR3 090KR3 090KR3 090KR3 090KR3 090KR3 090KR3 090KR3 090KR4 090KR4	PRT; 17 AA. Created) Last sequence upd Last annotation upd Last annotation upd T.; Craniata; Vertel T. Serjeantson; Secor 31; DB 4; BB26CAD60293722C BB26CAD60293722C BB26CAD60293722C BB26CAD60293722C BB26CAD60293722C
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11102222222222222222222222222222222222	RESULT 016310 ID 016310 DT 011-9 DT 011

Gaps

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"A prominent natural H-2 Kd ligand is derived from protein tyrosine kinase JAKI.";
                        Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=COL;
MEDLINE=96427339; PubMed=8830703;
WD S., de Lencastre H., Tomasz A.;
"Sigma-B, a putative operon encoding alternate sigma factor of
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MEDLINE-9339338; PubMed-8514334;
MEDLINE-9339338; Anitor A., Wilks A.F., Falk K., Rotzschke O., Rammensee H.G.;
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                                                                                                                                                                                                                 Length 16;
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                                                                                                                                                                   16 AA; 1946 MW; BBC625F8E4A4C8E7 CRC64;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTAN-2000 (TREMBLrel. 14, Last annotation update)
PROTEIN TYROSINE KINASE JAK1 (FRAGMENT).
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Staphylococcus aureus.
Bactlius/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=1280;
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50.0%; Pred. No. 9.2e+02;
ive 3; Mismatches 1;
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                                                                                                                  MEDLINE-94198758; PubMed-7764624;
Braun H.P., Kruft V., Schmitz U.K.;
Planta 193:99-106(1994).
SEQUENCE 16 AA; 1946 MW; BBC625E
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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SEQUENCE 22 AA; 2681 MW; D0
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Solanum tuberosum (Potato).
Mitochondrion.
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Best Local Similarity 25.0
Matches 4; Conservative
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Matches 4; Conserv
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                                                                           NCBI_TaxID=4113;
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2 HQYLPEDL 9
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Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
Taniguchi Y., Takehisa J., Debngui, M'Pandi M., M'Pele P., Harada Y.,
N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
Hayami M., Ichimura H., Parra J.H.;
"Generic Subtypes of HIV Type I Based on the vpu/env Sequences in
Republic of Congo-Brazzaville.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF127545; AAK84896.1;
                                                                 Sus scrofa (P1g).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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01-MAR-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYTOCHROME-C REDUCTASE 14 KDA SUBUNIT (EC 1.10.2.2) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                 Score 31; DB 6; Length 18;
Pred. No. 5.1e+02;
2; Mismatches 4; Indels
                                                                                                                                                                            Markmann A., Kresse H.;
"Regulation of YokC Differentiation.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF330200; AAL09466.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 AA; 2210 MW; 2A83642B89068236 CRC64;
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Last annotation update)
   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTEGRIN ALPHA 2 SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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Best Local Similarity 45.5
Matches 5; Conservative
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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TISSUE-CARDIOVASCULAR;
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SEQUENCE FROM N.A.
MEDLINE=96083592; PubMed=7493025;
Matkins H., Conner D., Thierfelder L., Jarcho J.A., MacRae C.,
McKenna W.J., Maron B.J., Seidman J.G., Seidman C.E.,
"Mutations in the cardiac myosin binding protein-C gene on chromosome
Il cause familial hypertrophic cardiomyopathy.";
Nat. Genet. 11:434-437(1995).
EMBL; S80805; AAB35661.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polounienko A., Blecher S.;
"Exon-intron structure of SMCX and SMCY genes in bovine and swine.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF135448; AAD34440.1; -.
NON TER 1 1 1
NON TER 17 17
SEQUENCE 17 AA; 1927 MW; 10351B0D516D16F0 CRC64;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                          Score 27; DB 4; Length 15;
Pred. No. 1.7e+03;
4; Mismatches 1; Indels
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SEQUENCE 18 AA; 1891 MW; 3EC842CE85A19C97 CRC64;
                                      4EDFDA937C826170 CRC64;
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Last sequence update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence v
01-NOV-1998 (TrEMBLrel. 08, Last annotation
CARDIAC MYOSIN BINDING PROTEIN (FRAGMENT).
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44.4%;
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                                      1646 MW;
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Matches 4; Conservative
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Best Local Similarity
Matches 5; Conserv
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15 AA;
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Q13665;
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"Single Nucleotide Polymorphism Analysis on Encoding Region of
"Extracellular Fatty Acid Binding Protein Genes and Their Associations
With the Fattiness Trait in Chicken.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF402001; AAK94062.1; -.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Staphylococcus aureus RNA polymerase: molecular cloning and DNA
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Bouvagnet P.;
"Chromosomal localization of human dynein heavy chain genes.";
Submitted (JAN.1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ132092; CAA10565.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28; DB 13; Length 11;
Pred. No. 8.7e+02;
0; Mismatches 1; Indels
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Pred. No. 1.4e+03;
0; Mismatches 2; Indels
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NON_TER 11 11
SEQUENCE 11 AA; 1277 MW; 873417F02B187AAA CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EXTRACELULAR FATTY ACID BINDING PROTEIN (FRAGMENT).
Gallus gallus (Chicken).
                                                                                      SEQUENCE 23 AA; 2541 MW; 7F47717B1767D34F CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
AXONEMAL DYNEIN, HEAVY CHAIN (FRAGMENT).
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                 sequencing.";
J. Bacteriol. 178:6036-6042(1996).
EMBL; Y09929; CAA71063.1; -.
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71.4%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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MEDLINE-21195339; PubMed-11297743;
MEDLINE-21195339; PubMed-11297743;
MEDLINE-21195339; PubMed-11297743;
Median K., Ambrosoft I., Elbling L., Micksche M., Berger W.;
A small upstream open reading frame causes inhibition of human major vault protein expression from a ubiquitous mRNA splice variant.";
PEBS Lett. 494:199-104(2001).
EMBL, AJ291367; CAC35315.1; -.
Hypothetical protein.
SEQUENCE 18 AA; 2179 MW; 5D06F9A3F11CB828 CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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               Length 17;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 2.2 KDA PROTEIN.
             Score 26.5; DB 6;
Pred. No. 2.4e+03;
2; Mismatches 5;
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             18.8%;
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EMBL; J02325; AAA47262.1; -.
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11 PHLP 14
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Pred. No. 4.7e+03;
1; Mismatches 2; Indels
 Length 21;
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NCBI_TaxID=103690;
                                   Indels
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Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                               Pohl B.;
Thesis (1999), University of Bonn, Botanical Institute.
EMBL; AJ132709; CAA10746.1; -.
NON_TER 23 23 23
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Score 26; DB 12; L
Pred. No. 3.5e+03;
3; Mismatches 3;
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MEDLINE-95112788; PubMed-7813418;
                                                                                                                                                                                                                                                                                                              Anabaena sp. (strain PCC 7120).
 18.4%;
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60.0%;
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                 Best Local Similarity 45.5
Matches 5; Conservative
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01-MAY-1999 (TrEMBLrel.
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01-MAR-2001 (TrEMBLrel.
ORF YBR090C (FRAGMENT).
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Jauniaux J.C., Jonniaux J.L., Kallesoe T., Kiesau P., Kirchrath L., Koetter P., Korol S., Liebl S., Logghe M., Lohan A.J.E., Louis E.J., Liebl S., Logghe M., Lohan A.J.E., Louis E.J., Liebl S., Liebl S., Logghe M., Lohan A.J.E., Louis E.J., Manchaupt G., Messenguy F., Miosaga T., Maleiar S., Masr F., Obermaier B., Perea J., Pierrad A., Paravandi E., Pohl F.M., Pohl T.M., Potier S., Proft M., Purnelle B., Ramezani Rad M., Rieger M., Rose M., Schaff-Gerstenschlaeger I., Scherens B., Schwarzlose C., Skala J., Slonimski P.P., Smits P.H.M., Van der Aart Q.J., Van Dyck L., Vassarotti A., Vetter I., Vierendeels F., Vissers S., Wagner G., Ge Westifosse P., Wolfe K.H., Equince of yeast chromosome II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea; Torpediniformes; Narcinoidei; Narcinidae; Discopyge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUB-ELECTRIC LOBE:
MEDLINE-95164564, PubMed-7860635;
Gesemann M., Denzer A.J., Ruegg M.A.;
"Acetylcholine receptor-aggregating activity of agrin isoforms and mapping of the active site.";
J. Cell Biol. 128:625-636(1995).
EMBL: U16146; AAA64486.1; --.
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Pred. No. 3.5e+03;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 3; Length 14; Pred. No. 3.3e+03; 1; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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50.0%;
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EMBL; 235957; CAA85041.1;
SGD; S0000294; YBR090C.
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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August 26, 2002, 10:18:42 ; Search time 79:43 Seconds (without alignments) 34.960 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                        747574 seqs, 111073796 residues
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1 CGETYYSRVTHPHLPKDIVRSIAKC
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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A_Geneseq_012802:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

AAY799	RESULT 1
2 X	AAY/9999 standard; Peptide; 25 AA.
O X	AAY79999;
E 2	15-MAY-2000 (first entry)
X E X	Optimised IgE-CH3 domain antigen peptide for dog IgE.
X X	Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
X X	antibody; allergy: allergy: dispase: immunication; helper T cell epitope;
X X	anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
SO	Canis sp.
s ×	Synthetic.
N X	WO9967293-A1.
O X	29-DEC-1999.
PF	21-JUN-1999; 99WO-US13959.
A X	20-JUN-1998; 98US-0100287.
PA X	(UNBI-) UNITED BIOMEDICAL INC.
PI	Wang CY, Walfield AM;
X D.X	WPI; 2000-160578/14.
PT	New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy -

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy $\mbox{\ \ -}$

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antigenic peptides (1). (1) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (1) induces polyclonal antibodies specific for a target effector site on the epsilon heavy chain of specific for a target effector site on the epsilon heavy chain of gress and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and may include cyclic constraints (asserted that the constraint may include cyclic constraints).
                                                                                                                                                                                                                                                             maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogentc) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                        present invention describes immunoglobulin E (IgE)-CH3 domain
           Claim 1; Page 99; 155pp; English
                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 25; Conser
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Synthetic.
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Best Local Si
Matches 25;
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                                                                                                                                                                                                                                                                                                                                      Sequence
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Length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy
                                                      Gaps
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                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Optimised IgE-CH3 domain antigen peptide for human IgE
Score 141; DB 21;
Pred. No. 1.2e-14;
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                                                      0; Mismatches
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                                                                                                        25
                                                                                                                                   Claim 1; Page 21; 155pp; English
                                                                                                        1 CGETYYSRVTHPHLPKDIVRSIAKC
                                                                                                                                                                                                                                                                                             AAY79998 standard; Peptide; 25
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                                                         Conservative
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specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermaititis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope conjugates of (I) that include a promiscuous T helper cell epitope arget epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe maximize cross-reactivity to the natural target. They induce safe con-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesteryl ester transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CDV receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic; plasmodium falciparum; circumsporozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                               Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                               76.6%; Score 108; DB 21; 72.0%; Pred. No. 1.3e-09; 11ve 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified human IgE CH3 domain, SEQ ID NO:92.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY91212 standard; peptide;
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Best Local Similarity 72.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                             25 AA;
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(UNBI-) UNITED BIOMEDICAL INC

WPI; 2000-160562/14.

Wang CY;

99WO-US13960. 98US-0100414.

21-JUN-1999; 20-JUN-1998;

W09966952-A1

29-DEC-1999.

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peptides comprising sometostatin, and a Th epitope. Sometostatin manuscons may be used to promote growth in livestock. AAY91208 is a human CD4 CDR2-like domain antigenic stre, and AAY91209-Y90210 are MVH Th epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV ceptope/CD4 CDR2 antigenic peptides which may be used to prevent HIV ceptope/CD4 CDR2 antigenic and AAY90212 is a modified version of a human IgE (immunoglobulin B) CH3 domain, and AAY90213-Y90219 are Th epitope/TgE CH3 antigenic peptides which may be used in the treatment of allergies. AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AAY91221-Y91221 comprise this peptide and a Th ceptope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target epitope and may be used in a malaria vaccine. AAY91228-Y9121 represent corp. CETP peptides and AAY91223-Y91241 are immunogens comprising a retreated are anteriosclerosis and cardiovascular disease. AAY91228-Y91257 are HIV-1 neutralishing B-cell epitopes, and AAY91252-Y91257 are HIV-1 neutralishing B-cell epitopes, and AAY91251-Y91251 and AAY91252-Y91257 are HIV-1 neutralishing B-cell epitopes, and AAY91251-Y91251 and HIV-1 B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
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luteinising hormone-releasing hormone; spermatogenesis; ovulation;
oestrus; sexual development; sex hormone; promiscous T helper epitope;
vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
breast cancer; endometriosis; boar taint; meat quality; immunocastration.
protein (CETP) or HIV epitopes, but more generally against any pathogen, Immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of luteinising hormone (LHRM) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and for immunocastration); for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous the functional in genetically diverse subjects) into an immunogen improves capacity to induce a subjects) into an immunogen response, resulting in production of antibodies against a target and partigen. The can replace carrier proteins and pathogen—derived T helper antipon.
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My191189 and AMY91199 are respectively an immunostimulatory invasin
protein epitope from Yersinia species, and hinge spacer peptide, both of
which may optionally be used in the antigenic peptides of the
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Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide immunogen containing luteinising hormone-releasing hormone antigen site and helper T cell epitope, for e.g. contraception and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes peptide immunogens comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 108; DB 21; Length 25;
Pred. No. 1.3e-09;
3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.6%;
72.0%;
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Best Local Similarity 72.0
Matches 18; Conservative
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Synthetic.
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WPI; 2000-160578/14
                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                          antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies and anti-asthmatic properties. (I) induces polyclonal antibodies and anti-asthmatic properties. (I) induces polyclonal antibodies as perefit for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermathis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. (conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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                                                                                                                 New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy \,\text{-}\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                 The present invention describes immunoglobulin E (IgE)-CH3 domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.5%; Score 105; DB 21; 176.0%; Pred. No. 3.8e-09; 11ve 0; Mismatches 6;
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                                    (UNBI-) UNITED BIOMEDICAL INC.
            98US-0100287.
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                                                              Wang CY, Walfield AM;
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                                                                                        WPI; 2000-160578/14
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Matches 19; Conserv
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            20-JUN-1998;
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antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of 1gE, and so preventing triggering and activation of mast cells and basophils and downregulation of 1gE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against 1gE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY7994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention.
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New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
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                                                                                                                                                                                                       The present invention describes immunoglobulin E (IgE)-CH3 domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.5%; Score 105; DB 21; Length 25; 72.0%; Pred. No. 3.8e-09; tive 4; Mismatches 3; Indels
                                                                                                                  Claim 1; Page 146; 155pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for immunization against allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canine immunoglobin E peptide 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 9; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95JP-0334381.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 72.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-389423/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-1995;
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IgE antibody. The anti-canine IgE antibody can be used for the diagnosis

AAY50894 standard; peptide; 17 AA.

AAY50894;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
epitope; prophylaxis; treatment; mimotope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binding proteins used for treatment or prophylaxis of canine allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody 15A.2 binding peptide 10 from PhDc7c phage display library.
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                                                                                                                                                           Length 20;
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                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                           DB 18;
9.9e-08;
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Pred. No. 2e-06;
); Mismatches
                                                                                                                                                                                                                Mismatches
                                                                                                                                                           Score 95;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Francoeur G;
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94.1%;
                                                                                                                                                                                                                                                                                                99EP-0107035
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                                                                                                                                                                                                                                                               6 YSRVTHPHLPKDIVRSIAK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mermer B,
                        of canine allergies
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                                                                                                                                                        Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                             20 AA;
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30-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                          Sequence
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Matches
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AAYSO8
AAYSO893
AAYSO
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RESULT

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This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound igE, and which doesn't bind to IgE when the igE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound igE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.

ANY50876-Y50900 represent peptide mimotopes used in the method of the
                                                                                                               Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
                                                                                                                                                                                                                                                                                                                                                                             Binding proteins used for treatment or prophylaxis of canine allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds; receptor-binding; binding determinant sequence; anti-IgE antibody; allergic disease.
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Pred. No. 2e-06;
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                                                                                       Antibody 15A.2 canine IgE binding epitope 1.
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                                                                                                                                                                                                                                                                                                                           Francoeur G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.0%;
94.1%;
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                                                                                                                                                                                                                                                           98US-0058331
99US-0281760
                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IgE peptide antagonist
                                                                                                                                                                                                                                                                                                  (IDEX-) IDEXX LAB INC.
                                                                                                                                                                                                                                                                                                                           Mermer B,
                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-040833/04.
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nes 16; Conser
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                                                               24-FEB-2000
                                                                                                                                                                                                                                  09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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30-MAR-1999;
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                                                                                                                                                                                                                                                                                                                          Lawton R,
                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
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Matches
AAY42585
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WPI; 1999-579941/49.
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                 24 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09967293-A1
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                       AAY80001;
                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                   The invention provides immunoglobulin E (IgE) antagonists comprising one or more of the FcepsilonRI receptor-binding determinant sites of human IgE. The antagonists include IgE variants comprising an immunoglobulin template and binding determinant sequences (bds) CDbds, EFbds and the sequence shown in AAY42581. The CDbds (CD loop binding determinant sequence) are selected from the sequences shown in AAY42567. and the EFbds (EF loop binding determinant sequences are selected from sequences shown in AAY42578-Y42580. The variants are useful in raising and screening anti-IgE antibodies, in the isolation and purification of FeepsilonRI receptor and in the treatment and prophylaxis of allergic
                                                                                                                                   Immunoglobulin E variants as peptide antagonists useful for raising and screening anti-immunoglobulin E (IgE) antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment of allergic
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bdi
receptor-binding; binding determinant sequence; anti-IgE antibody;
allergic disease.
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Pred. No. 0.00037;
3; Mismatches 3; Indels
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                            94US-0232539
                                               91US-0744768
94US-0178583
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94US-0178583
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IgE peptide antagonist.
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                                                                            (GETH ) GENENTECH INC.
                                                                                                                 WPI; 1999-579941/49.
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                        22 AA;
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                            21-APR-1994;
                                                14-AUG-1991;
                                                         07-JAN-1994;
                                                                                               Jardieu PM,
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        12-OCT-1999
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                                                                                                                                                                                                                                                                                                                          Seguence
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                                                                                                                                                                                                                                                                                       comprising one
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Immunoglobulin E variants as peptide antagonists useful for raising and screening anti-immunoglobulin E (IGE) antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin B; IgB; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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pred. No. 0.0004;
3; Mismatches 3; Indels
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                                                                                                                                                                                                           Disclosure; Column 9; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY80001 standard; Peptide; 25 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US13959.
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and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allerques, e.g. food allerques, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY70994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE behan the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.

AMY50076-Y50900 represent peptide mimotopes used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
epitope; prophylaxis; treatment; mimotope.
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                                                                                                                                                                                                                                                                                                                                                                              46.8%; Score 66; DB 21; 56.0%; Pred. No. 0.0035;
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99US-0281760.
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Best Local Similarity
Matches 14; Conserv
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30-MAR-1999;
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ANY50876-Y50900 represent peptide mimotopes used in the method of the
                                                                                                                                                                                                                                          Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
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Score 63; DB 21; Length 17; Pred. No. 0.0065;
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                          Mismatches
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                                                                                                                                          AAY50898 standard; peptide; 17
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70.6%;
  44.78;
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99US-0281760.
             78.68;
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                                                                                                                                                                                             (first entry)
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                          Conservative
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             Local Similarity
nes 11; Conserv
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Matches 12; Conserv
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30-MAR-1999;
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Matches
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AAY50895;

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                                                                               Canine, allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
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Pred. No. 0.019;
3; Mismatches 1; Indels
                                                     Antibody 15A.2 human IgE binding epitope 1.
                                                                                                                                                                                                                                                                                                                    Francoeur G;
                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 7; 30pp; English
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Best Local Similarity 71.4%;
Matches 10; Conservative
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99US-0281760
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                          24-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                       (IDEX-) IDEXX LAB INC.
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30-MAR-1999;
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                                                                                                                             Synthetic.
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Search completed: August 26, 2002, 10:18:42 Job time: 698 sec

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CLASSIFICATION: 4.4

ATTORNEY AGENT INFORMATION:
NAME: MAILA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPHONE: 212-751-649
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 anin acids
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APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
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Best Local Similarity 72.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-09-100-414B-95
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Sequence 95, Appl
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Sequence 3
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-303-323-95
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US-08-223-5390-19
US-08-218-025A-186
US-08-077-797A-14
US-08-077-797A-14
US-08-077-797B-9
US-08-11-307B-9
US-08-311-307B-9
US-08-317-759B-313
US-08-877-759B-313
US-08-877-759B-313
US-08-877-759B-313
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US-08-195-006-27
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US-08-185-008-008-008-008-008-281-90-80
US-08-284-9518-3
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141
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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76.6%; Score 108; DB 3; Length 25; 72.0%; Pred. No. 4.6e-11; Live 3; Mismatches 4; Indels

amino acid

-029-348-6 Segmence	-324-14		-	US-08-602-999A-226 Seguence	-	4				371		ı	US-08-466-763-9	6	•		976-358-18
4 US-09-029	3 US-08-		1 US-08-									_				1 US-07-	1 US-07-
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21.3	21.3	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6
30	30	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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Score 72; DB 2; Length 22;
Pred. No. 2.8e-05;
3; Mismatches 3; Indels
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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/178583
FILING APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 07/3AN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AGG-1991
ATTORNEY/AGRIT INFORMATION:
NAME: SVODOda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 90118P3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 132-539D-20
; Sequence 20, Application US/08232539D
; Patent No. 5965700:
; General INFORMATION:
   APPLICANT: Presta, Leonard G.
   APPLICANT: Jardieu, Paula M.
   TITLE OF INVENTION: IGE Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
                              CURANIA .....
CURASIE/COATION NUMBER: US/UB/22/----
FILING DATE: 21-Apr-1994
CLASSIE/COATION 530
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION NUMBER: 07/744768
FILING DATE: 14-AGG-1991
APPLICATION NUMBER: 39,044
REFINENCE/COAGA, Craig G. REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 90/18P: TELEPHONE: 650/225-1489
TELEPHONE: 650/225-1489
TELEPHONE: 650/225-1489
TELEPHONE: 650/225-1489
TELEPHONE: 22 mmino acids
TYPE: Anino Acid
TYPE: Anino Acid
                                                                                                                                                                                                                                                                                                              P0718P3
WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GETYYSRVTHPHLPKDIV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 GETYQCRVTHPHLPRALM 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 51.1
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                650/952-9881
                    CURRENT APPLICATION DATA APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-08-232-539D-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                       US-00-303-323-95

Sequence 95, Application US/09303323

Patent No. 628987

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: NOVEL LHRH PEPTIDE

TITLE OF INVENTION: IMMUNGENS

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: IgE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
                                                                                                                                                                         CITY: NW YORK
STATE: NY
STATE: NY
                                                                                                                                                                                                                                                                                                                                       ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. LIN
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-232-539D-19
; Sequence 19, Application US/08232539D
Patent No. 5965709
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 95: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                       RY: USA
10154-0054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94080
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                                                                                                                                                                                                                                                                                                                         COUNTRY:
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Gaps

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Gaps
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Patent No. 5556744
GENERAL INFORMATION:
APPLICANT: Weiner, David B.
APPLICANT: Williams, William V.
TITLE OF INVENTION: Methods and Compositions for Diagnosing
TITLE OF INVENTION: and Treating Certain HIV Infected Patients
NUMBER OF SEQUENCES:
                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                      Score 72; DB %; Length 24;
Pred. No. 3.1e.05;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Howson and Howson STREET: P.O. Box 457, 321 No. 5556744ristown Road CITY: Spring House CITY: Spring House COUNTE: Pennsylvania COUNTE: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWALES SISTEM: PC-UCS/MS-UCS
SOFTWALES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,025A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 424
APPLICATION DATA:
APPLICATION NUMBER: US 07/891,451
FILING DATE: 29-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bak, Mary E.
REGIETRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 43.8%;
Local Similarity 43.8%;
Annual Conservative
                                                                                                                                                                                                                                  2 GETYYSRVTHPHLPKDIV 19
                                                                                                                                                                                                                                                        7 GETYQCRVTHPHLPRALM 24
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                    Query Match 51.19
Best Local Similarity 66.79
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGETYYSRVTHPHLPK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-218-025A-186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                Linear
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                                                                                                                                                                                                                                                                                                                                              US-08-218-025A-186
                                                                          ; TOPOLOGY:
US-08-232-539D-20
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Gaps
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| Sequence 14, Application US/08077797A
| Patent No. 5679548
| GENERAL INFORMATION:
| APPLICANT: Barbas, Carlos F.
| APPLICANT: Cerner, Richard A.
| TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL
| TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF
| NUMBER OF SEQUENCES: 65
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: The Scripps Research Institute, Office of
| ADDRESSEE: Patent Counsel
| STREET: 10666 No. 5679548th Torrey Pines Road, TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
Sequence 52, Application US/09017205
Patent No. 5965357
CENERAL INFORMATION:
PAPLICANT: Marsden, Howard S
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                 ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5965357th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/017,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide from HSV-2 glycoprotein G FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 2;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US/09/017,205
02-FEB-1998
                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29,009
REFERENCE/CDCKET NUMBER: 604-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)815-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.5%;
75.0%;
                                                                                                                                                                                                                                                                                   ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.v.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                          CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         La Jolla
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7 THPHGPAD 14
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US-08-077-797A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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RESULT

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APPLICANT: Margosian, Linda
APPLICANT: Margosian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
TITLE OF INVENTION: Development in Plants
FILE REFERENCE: 023070-08612008
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER PELING DATE: 1998-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAPLICANT: Talmadge, James E.

TITLE OF INVENTION: Anti-inflammatory Polypeptide
TITLE OF INVENTION: Antagonists of Human Interleukin-8
NUMBER OF SEQUENCES: 11
CORRESPONDEC ADDRESS:
ADDRESSEE: 1601 Market Street
CITY: Philadelphia
STRATE: PA
COUNTR: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Datentin Release #1.0, Version #1.30
COMPUTER: Patentin Release #1.0, Version #1.30
COMPUTER: Patentin Release #1.0, Version #1.30
COMPUTER: DATE: 28-UN-1996
CLASSIFICATION NUMBER: 28-UN-1996
TILING DATE: 28-UN-1996
CLASSIFICATION NUMBER: 57,643
REGISTRATION NUMBER: 63086FWC
TELECOMMUNICATION NUMBER: (215)563-4040
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 4; Length 18; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                        Sequence 298, Application US/09177249; Patent No. 6229064; GENERAL INFORMATION: APPLICANT: Fischer, Robert L. APPLICANT: Kiyosue, Tomohiro APPLICANT: Yadegari, Ramin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08671094B Patent No. 5912232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 298
LENGTH: 18
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Best Local Similarity 50.v.
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT CRGANISM: Arabidopsis sp. US-09-177-249-298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 KDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :||:: ||
2 KSVVRNVQKC 11
                                                                       US-09-177-249-298
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US-08-671-094B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL ILE CHE CHENCENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL
TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF
TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF
NUMBER OF SEQUENCES: 65
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01238
FILING DATE: 01-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,797
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,566
FILING DATE: 02-FEB-1993
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34.5; DB 5; Length 16;
Pred. No. 24;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 16;
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34.5; DB
Pred. No. 24;
3; Mismatches
                                                               FILING DATE: 14-UNN-1993

CLASSIFICATION: 435

PRIOR APPLICATION A 435

PRIOR APPLICATION DATE: 0.08/012,566

FILING DATE: 0.2-FEB-1993

ATTORNEY/AGENT INFORMATION:
NAME: FILLING, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCR1276P

TELECHOMUNICATION INFORMATION:
TELECHOMUS: 619-554-6312

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids

TYPE: amino acids
                                           APPLICATION NUMBER: US/08/077,797A
FILING DATE: 14-JUN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application PC/TUS9401238 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.5%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 24.5%;
Best Local Similarity 43.8%;
Matches 7; Conservative
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1 GDTHRGHLRH-HLPHD 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GETYYSRVTHPHLPKD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
PCT-US94-01238-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GETYYSRVTHPHLPKD 17
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Gaps

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us-09-701-623c-6.closed.rai

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not relevant
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62.5%;
                                                                  Query Match
Best Local Similarity 53.0
...has 7; Conservative
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                                                                                                                                                                                                                     1 CGETYYSRVTHPH 13
                                                                                                                                                                                                                                                        | :| ||: |||
6 CIKT-YSKPFHPH 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino ac1d
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Best Local Similarity
Matches 5; Conserv
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10 YSKPFHPH 17
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
         US-08-311-307B-9
                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-08-847-696A-9
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                                                                                                                                                                                                                                                              , OTHER INFORMATION: /note= "The cysteine residues ; OTHER INFORMATION: /note= "The cysteine residues ; OTHER INFORMATION: may be substituted with aminobutyric acid, homocysteine or ; OTHER INFORMATION: diaminosuberic acid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "The cysteine residues may
be substituted with aminobutyic acid, homocysteine or
diaminosuberic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: DADRESSE: DAGRATE: DAG
                                                  TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGETYYSRVTHPH 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :| ||: |||
4 CIKT-YSKPFHPH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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NAME/KEY: Modified-site

LOCATION: 4..6

OTHER INFORMATION: /note= "The Xaa in positions 4 and 6

OTHER INFORMATION: in the peptide may be aminobutyric acid, homocysteine, cys;

OTHER INFORMATION: diaminosuberic acid."
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                                             Gaps
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                                                                                                                                                                                                                                                                                                      APPLICANT: Talmadge, James E. TITLE OF INVENTION: Polypeptide Agonist For Human Interleukin-8 NUMBER OF SEQUENCES: 12
                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
  Length 17;
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Pred. No. 65;
                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTER. USA

ZIP: 19103-2307

COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,696A
FILING DATE: 28-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/311,307
FILING DATE: 3-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street
CITY: Philadelphia
                                           3,
  DB 1;
Score 32.5; DE
Pred. No. 54;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Rigaut, Kathleen D.
REGISTRATION NUMBER: P 43,047
REFERENCE/DOCKET NUMBER: 63085C
TELEPAN: (215)563-400
TELEPAN: (215)563-4044
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         Sequence 9, Application US/08847696A Patent No. 5877276 GENERAL INFORMATION:
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1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION NUMBER: PCT/0895/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION 1435
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: RPMS 101 CON
TELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8795
INFORMATION FOR SED ID NO: 313:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TTYPE: amino acids
TYPE: mino acids
TYPE: APPLICATION CON ACIDS OF THE CONTROL CHARACTERISTICS:
TYPE: APPLICATION ACIDS OF THE CONTROL CHARACTERISTICS:
TYPE: ADMINISTED ACIDS OF THE CONTROL CHARACTERISTICS:
TELEGRAPH: APPLICATION ACIDS OF THE CONTROL CHARACTERISTICS:
TELEGRAPH: APPLICATION ACIDS OF THE CONTROL CHARACTERISTICS:
TELEGRAPH: APPLICATION ACIDS OF THE CONTROL CHARACTERISTICS:
THE CONTROL CHARA
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STATE: Georgia
COUNTRY: USA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISA
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31.5; DB 3;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-201-945-313
US-09-201-945-313
Sequence 313, Application US/09201945
Patent No. 6342215
GENRAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INFORMION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPMS 101
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.3%;
50.0%;
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Best Local Similarity 50.0.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-871-355A-313
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                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY USA

ZIP: 30309-3450

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/637,759B

FILING DATE: 03-MAX-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB95/02875

FILING DATE: 11-DEC 1995

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31.5; DB 2;
Pred. No. 1.2e+02;
3; Mismatches 3;
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Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
INFORMATION FOR SEC ID NO: 313:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                         CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                       US-08-637-759B-313
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## TELEPHONE: (404) 873-8794
## TELEFAX: (404) 873-8795
## TELEFAX: (404) 8
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ή:

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Mon Aug 26 11:09:26 2002
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 26, 2002, 10:20:41; Search time 43.94 Seconds (without alignments) 54.671 Million cell updates/sec Run on:

US-09-701-623C-7 145 1 CGEGYQSRVDHPHFPKPIVRSITKC

Title: Perfect score: Sequence:

25

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

4981 Total number of hits satisfying chosen parametars:

Minimum DB seq length: 0 Maximum DB seq length: 25

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	alpha-amvlase inhi	as	high conductance c	trýptophyllin-13 -	paralytic peptide		paralytic peptide	tryptophyllin-rela	hypothetical MTC01	carboxylesterase (thrombopoietin rec	acid ribonuclease	N4-(beta-N-acetyld	mannose-1-phosphat	serum albumin - do	T-cell receptor al	mannose-1-phosphat	cystathionine beta	hypothetical prote	n (EC 3	glue protein - Cal	gene HEXA protein	p7 protein - human	probable acr-2 req	cenA protein (IqA1	serine proteinase	Iq H chain V-D-J r	hypothetical prote	Ξ
SUMMARIES	ID	S48156	S26664	B53145	A05174	E39855	C39855	D39855	S21152	509363	S09025	I78841	A41439	JN0910	A47415	S29749	S03456	B47415	151879	T02624	PN0133	A61093	154351	S41390	S72535	140692 .	A60704	PH1597	0	B49254
	DB	7	~	~	7	7	ď	~	7	4	~	7	~	7	~	C3	~	7	7	7	~	~	7	7	~	7	7	~	~	7
	Query Match Length	23	18	19	13	23	23	23	13	24	20	18	20	22	23	24	25	13	16	19	20	20	21	23	23	25	25	14	16	18
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ALIGNMENTS

RESULT

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alpha-amylase inhibitor - rye
C;Species: Secale cereale (rye)
C;Date: 07-May-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C;Accession: S48156
By Sarcia-Casado, G.; Sanchez-Monge, R.; Lopez-Otin, C.; Salcedo, G.
Bur. J. Biochem. 224, 525-531, 1994
A;Title: Rye inhibitors of animal alpha-amylases show different specifities, aggregat
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                                                                                                                                                                                      A,Accession: S48156
A;Status: preliminary
A;Molecule type: protein
C;Superfamily: wheat alpha-amylase inhibitor
C;Keywords: alpha-amylase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GEGYQSRVDHPHFPKPIVRSI 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GEWCWPGMGHPMYPFPRCRAL 23
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Best Local Similarity 33.3%
Conservative
T; Conservative
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microtubule-associated protein tau - human c; Species: Homo sapiens (man)
C; Accession: S26664
R; Andreadis, A.; Brown, W.M.; Kosik, K.S.
Biochemistry 31, 10626-10633, 1992
A; Title: Structure and novel exons of the human tau gene.
A; Reference number: S26662; MUID: 93041757
A; Accession: S26664
A; Status: preliminary; nucleic acid sequence not shown; translation not shown RESULT S26664

A; Molecule type: DNA A; Residues: 1-18 <AND>

A;Cross-references: EMBL:X61375 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991

ö Gaps ; Query Match
20.0%; Score 29; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels

: | | | | | 4 KSREDHP 10 6 QSRVDHP 12 ò q

Gaps

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Indels

Pred. No. 1.2e+03;

50.0%;

0; Mismatches

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Best Local Similarity 50.0
Matches 5; Conservative
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J. Biol. Chem. 269, 3921-3924, 1994
A;Title: Subunit composition of the high conductance calcium-activated potassium channel
A;Reference number: A53145; MUID:94140798
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    paralytic peptide III - beet armyworm
C;Species: Spodoptera exigua (beet armyworm)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C;Accession: E39855
R;Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.
A; Biol. Chem. 266, 12873-12877, 1991
A;Title: Isolation and identification of paralytic peptides from hemolymph of the lepidc
A;Reference number: A39855; MUID:91302298
                                                                                                    high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragment) c. Species: Bos primigenius taurus (cattle) C;Bate: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Jul-2001 C;Accession: B53145
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C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Aug-2000
C;Accession: A05174
R;Montecucofil, P.C.; Gozzini, L.; Erspamer, V.
Int. J. Pept: Protein Res. 27, 175-182, 1986
A;Reference number: A05174
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C;Keywords: pyroglutamic acid; skin
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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A;Residues: 1-19 KKNA>
A;Note: sequence extracted from NCBI backbone (NCBIP:144547)
C;Superfamily: fruit fly calcium-activated potassium channel slo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.0%; Score 29; DB 2; Length 19; 54.5%; Pred. No. 6.7e+02; ive 1; Mismatches 4; Indels
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44.4%; Pred. No. 6.2e+02;
ive 3; Mismatches 2; Indels
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A;Molecule type: protein
A;Residugs: 1-23 <SKI>
C;Superfamily: paralytic peptide I
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Best Local Similarity 44.4
Matches 4; Conservative
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Matches 6; Conserv
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2 EKPYWPPPI 10
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Length 23;

DB 2;

19.3%; Score 28;

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Cispedies: Spodoptera exigua (beet armyworm)
Cispedies: Spodoptera exigua (beet armyworm)
Cispedies: Spodoptera exigua (beet armyworm)
Cispedies: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
Ciscossion: C39655
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B. J. Biol. Chem. 266, 12873-12877, 1991
A:Title: Isolation and identification of paralytic peptides from hemolymph of the lep A:Reference number: A39855; MUID:91302298
A:Reference number: A39855; MUID:91302298
A:Status: preliminary
A:Wolecule type: protein
A:Residues: 1-23 < SKI>
C:Superfamily: paralytic peptide I
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C;Species: Spodoptera exigua (beet armyworm)
C;Species: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C;Accession: D38855
R;Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B J. Biol. Chem. 266, 12873-12877, 1991
A;Title: Isolation and identification of paralytic peptides from hemolymph of the lep A;Reference number: A39855; MUID:91302298
A;Status: preliminary
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R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, A;Tile: 302, 151-154, 1992
A;Reference number: S21152; MUID:92339502
A;Acession: S21152
A;Molecule type: protein
A;Ressidues: 1-13 <MIG>
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C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
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Pred. No. 1.2e+03;
0; Mismatches 5; Indels
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Pred. No. 1.2e+03;
0; Mismatches 5;
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A; Residues: 1-23 <SKI>
C; Superfamily: paralytic peptide I
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50.0%;
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Best Local Similarity
1 CGEGYQSRVD 10
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7 CTPGYORTAD 16
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Mon Aug 26 11:09:26 2002

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RESULT 13
JN0910
N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) alpha chain - Flavobacter
N;Alternate names: glycosylasparaginase; N4-(N-acetyl-beta-glucosaminyl-)-L-asparagin
C;Species: Flavobacterium meningosepticum
C;Species: Plavobacterium meningosepticum
C;Species: I4-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 17-Mar-1999
C;Accession: JN0910
R;Tarcentino, A.L.; Plummer Jr., T.H.
Biochem. Blophys. Res. Commun. 197, 179-186, 1993
A;Title: The first demonstration of a procaryotic glycosylasparaginase.
A;Reference number: JN0910; MUID:94071939
A;Accession: JN0910
A;Residues: J-02-CARA>
C;Comment: This heterodimeric enzyme is the counterpart to a lysosomal amidase/amidoh
gine-linked glycans.
C;Keywords: heterodimer; hydrolase
thrombopoietin receptor - mouse (fragment)
C; Species: Mus sp. (mouse)
C; Species: Mus sp. (mouse)
C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C; Accession: I78841
R; Alexander, W.S.; Dunn, A.R.
Oncogene 10, 795-803, 1995
Oncogene 10, 795-803, 1995
A; Title: Structure and transcription of the genomic locus encoding murine c-Mpl, a re A; Reference number: I78830, MUID:95166571
A; Reference number: I78841
A; Accession: I78841
A; Molecule type: mRNA
A; Residues: 1-18 < RES>
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acid ribonuclease (EC 3.1...) - bovine (fragment)
acid ribonuclease (EC 3.1...) - bovine (fragment)
c.Species: Bos primiganius taurus (cattle)
c.Saccession: A41439
J. Biochem. 103, 267-273, 1988
A.Fitle: Purification of acid ribonucleases from bovine spleen.
A.Reference number: A41439; MUID:88227899
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C;Genetics:
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Pred. No. 1.7e+03;
1; Mismatches 3; Indels
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Pred. No. 1.9e+03;
2; Mismatches 2; Indels
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Pred. No. 2.2e+03;
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Best Local Similarity 50.0
Matches 4; Conservative
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A;Molecule type: protein
A;Residues: 1-20 <OHG>
C;Keywords: hydrolase
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9 HLYFPKDL 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical MTCO1/MTCYB mutant fusion protein "human mitochondrion (fragment) C.Species: mitochondrion Homo sapiens (man) C.Species: mitochondrion Homo sapiens (man) C.Date: 21-Nov-1993 #sequence_revision 14-Aug-1997 #text_change 20-Apr-2000 C.Date: 21-Nov-199363 Requence_revision 14-Aug-1997 #text_change 20-Apr-2000 C.Pocusion: 209363 R.Poulton, J.; Deadman, M.E.; Gardiner, R.M. Nucleic Acids Res. 17, 10223-10229, 1989 A.Title: Tandem direct duplications of mitochondrial DNA in mitochondrial myopathy: anal A.Title: Tandem direct duplications of mitochondrial DNA in mitochondrial myopathy: anal A.Molecule type: DNA A.Molecule type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
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C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 30-5ep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C; Accession: S09025
R; Hosokawa, M; Maki, T; Satch, T.
Arch. Biochem. Biophys. 277, 219-227, 1990
A; Title: Characterization of molecular species of liver microsomal carboxylesterases A; Reference number: S09021; MUID: 90179180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
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                                                                                                                                  Score 27; DB 2; Length 13;
Pred. No. 8.86:+02;
2; Mismatches 3; Indels
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C;Keywords: carboxylic ester hydrolase
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Pred. No. 1.62+03;
2; Mismatches 4;
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A,Genetic code: SGCI
C,Reywords: Idusion protein; mitochondrion
T,4/Region: cytochrome-c oxidase chain I
F;5-24/Region: cytochrome b (+2 frame shifted)
   A:Experimental source: skin
C;Superfamily: unassigned animal peptides
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31.2%;
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Best Local Similarity 44.4%;
Matches 4; Conservative
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Best Local Similarity 31.2
Matches 5; Conservative
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Best Local Similarity 41.7
Matches 5; Conservative
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2 EKPFYPPPI 10
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mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 37K beta chain - pig (fragment)
N:Alternate names: GDP-mannose pyrophosphorylase 37K beta chain
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 25-Feb-1994 #sequence_revision 12-Aug-1996 #text_change 13-Sep-1998
C;Accession: A47415
R;Szumlo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.
J. Biol. Chem. 268, 17943-17950, 1993
A;Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and utilization of the constant of the constan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP A; Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ac C; Superfamily: mannose-1-phosphate guanylyltransferase C; Keywords: nucleotidyltransferase
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: S29749
R;Dixon, J.W.; Sarkar B.
R;Dixon, J.W.; Sarkar B.
A;Dixon, J.W.; Sarkar B.
A;Title: Isolation, amino acid sequence and copper(II)-binding properties of peptide (1-A;Reference number: S29749; MUID:75011422
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A; Accession: A47415
A; Molecule type: protein
A; Residues: 1-23 <S2U>
A; Note: sequence extracted from NCBI backbone (NCBIP:136438)
C; Complex: The enzyme appears to be a heterodimer of alpha and beta chains.
C; Function:
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    Indels
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 1.24 < DIX>
C; Superfamily: serum albumin repeat homology
2;
    Mismatches
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Matches 7; Conservative
6; Conservative
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3 KPIVLSTT 10
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| EAYKSEIAH 9
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15.JUL-1999 (Rel. 38, Last sequence update)
15.JUL-1999 (Rel. 38, Last annotation update)
15.JUL-1999 (Rel. 38, Last annotation update)
Cardioactive peptide CAP23.
Spodoptera eridania (Southern armyworm).
Spodoptera eridania (Southern armyworm).
PEUKATYOTA: Medetaxoa; Arthropoda; Tracheata; Hexapoda; Insecta;
PECTYGOTA: Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                             01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
11-NPLOPHYLLIn-13.
Phyllomedusa rohdei (Rohde's leaf frog).
Phyllomedusa Ratazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylldae; Phyllomedusa.
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Q02210
P28879
                             P35451
P30251
P30252
P37154
P12358
P81050
P02807
P056973
P01519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Montecucchi P.C., Gozzini L., Erspamer V.;
Primary structure determination of a tryptophan-containing
Tridecapeptide from Phyllomedusa rohdei.";
Int. J. Pept. Protein Res. 27:175-182(1986).
1- TISSUE SPECIFICITY: SECRETED.
PIR; A05174, A05174.
MOD_RES.
1 1 PYRROLIDONE CARDAVITA ACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB 1; Length 13;
Pred. No. 2.5e+02;
3; Mismatches 2; Indels
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                             MII7_BOVIN
PAPI_HELVI
PAP2_HELVI
LCA_FELCA
PSBR_WHEAT
                                                                                                           ANT3_MESAU
MT_NEUCR
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CXA1_CONGE
DCMM_PSECA
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MEDLINE=99196260; PubMed=10098624;
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13 AA; 1646 MW;
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 Peptides 20:53-61(1999)
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2 EKPYWPPPI 10
NCBI_TaxID-8394;
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ID TP13_PHYRO
AC P04096;
YT 01-***
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P56683;
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                               Compugen Ltd
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              GenCore version 4.5 Copyright (c) 1993 - 2000 Com
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                                                                                                         August 26, 2002, 10:30:17;
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MK3_PALPR
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PAP2_SPOEX
PAP3_SPOEX
MK2B_PALPR
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Gapop 10.0 , Gapext 0.5
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seq length: 25
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Paralytic peptide II (PP II).
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P30257;
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DISULFID
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 HELIOCHIS VIRESCENS.;
J. BALO. (Chem. 266.12873-12877 (1991).
1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
HEMOLYWHY LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
PIR; C39855; C39855.
                              AT HIGH DOSES.
-1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                      CONCENTRATIONS OF PEPTIDE AND CHRONOTROPIC AND INOTROPIC EFFECTS
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
FUNCTION: HAS EXCITATORY EFFECTS ON A SEMI-ISOLATED HEART FROM LARVAL MANDUCA SEXTA, CAUSING AN INOTROPIC EFFECT AT LOW
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                                                                                                                            Score 28; DB 1; Length 23;
Pred. No. 4.5e+02;
0; Mismatches 5; Indels
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                                                                                     BY SIMILARITY.
0A96D72A70855AE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
0A96D1F600855AE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28; DB 1; Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Spodoptera exigua (Beet armyworm).
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Last sequence update)
Last annotation update)
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MEDLINE-91302298; PubMed-2071576;
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Pfam; PF02425; GBP_PSP; 1.
                                                   HSSP; O61704; 185N.
InterPro; 1PR003463; GBP_PSP.
Pfam; PF02425; GBP_PSP; 1.
DISULFID 7 19
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50.0%;
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50.0%;
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2451 MW;
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                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
                                                                                                                                                                        1 CGEGYQSRVD 10
                                                                                                                                                                                            7 CTPGYORTAD 16
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Pa0256;
Ol_APR-1993 (
01-APR-1993 (
15-JUL-1999 (
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P30255;
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                                                                                              SEQUENCE
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PAP1_SPOEX
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PAP2_SPOEX
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Eukaryota; Metazoa; Arthrooda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla;
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryyota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla; Noctucidae; Noctucidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                 Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
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0A96CB4600855AE0 CRC64;
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0A96CB5EB7D55AE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.3%; Score 28; DB 1; Le 50.0%; Pred. No. 4.5e+02; ive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18-zulytic peptide III (PP III).
Spodoptera exigua (Beet armyworm).
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MEDLINE-91302298; PubMed-2071576;
                                                                                                                                                MEDLINE-91302298; PubMed-2071576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003463; GBP_PSP. Pfam; PF02425; GBP_PSP; 1.
                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003463; GBP_PSP.
Pfam; PF02425; GBP_PSP; 1.
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2505 MW;
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23 AA; 2477 MW;
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Matches 5; Conservative
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23 AA;
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8 RVDHPHFPKPI 18
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2 RFEHENLPORI 12
              Query Match
Best Local Similarity
Matches 4; Conserv
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nes 4; Conserv
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4 PQPFVR 9
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P56870;
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P82176;
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                                                                                                                            MCA2_RHOOP
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IMPI_GALME
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                        Gaps
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                                                                                                                                                                                                                                                                                             Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
"The inducible antibacterial peptides of the hemipteran insect
Palomena prasina. Identification of a unique family of proline-rich
peptides and of a novel insect defensin.";
J. Insect Physiol. 42:81-89(1996).
-!-PUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, FUNCTION, AND AMIDATION.
Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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Pterygota, Neoptera, Paraneoptera, Hemiptena, Euhemiptera,
Heteroptera, Panheteroptera, Pentatomomorpha, Pentatomoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                     17.6%; Score 25.5; DB 1; Length 16; 40.0%; Pred. No. 7.20±402; Live 4; Mismatches 4; Indels
  Length 23;
Score 28; DB 1; Length 23;
Pred. No. 4.5t+02;
); Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Panagrellus redivivus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Panagrolaimidae; Panagrellus.
                                                                                                                                                                                                                                                                                                                                                                                      Antibiotic; Insect immunity.
SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;
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CB13E4C9D776C'76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation upda:e)
FMRFamide-like neuropeptide PF6 (NGAPQPFVR:?-amide).
                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                           16 AM.
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0
19.3%;
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Query Match 19.3
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                          STANDARD;
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MOD_RES 10 10
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1 VDKPDYRPRPWPRNM 15
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NCBI_TaxID=55431;
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Best Local Similarity
                                             1 CGEGYQSRVD 10
                                                                 7 CTPGYORTAD 16
                                                                                                                                                                                                                                                                                      TISSUE-Hemolymph;
                                                                                                                                                                                              Palomena prasina.
                                                                                                                                                                                 Metalnikowin IIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-6233;
                                                                                                                                                                                                                                                                                                                                                                   BACTERIA
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P82660;
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                                                                                                                         MK2B_PALPR
P80410;
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                                                                                                              MK2B_PALPR
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THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
PRODUCTS AND AS IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodococcus opacus 1CP.";
J. Bacteriol. 180:3503-3508(1998).
-!- CATALYTIC ACTIVITY: 3-oxoadipate + NAD(P)(+) = 2-maleylacetate +
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Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Pyraloidea; Pyralidae; Galleriinae; Galleria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.; "Characterization of a maleylacetate reductase encoding region from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodococcus opacus (Nocardia opaca).
Bacteria, Firmicutes; Actinobacteria, Actinomycetales; Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
NCBI_TaxID=37919;
                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative maleylacetate reductase II (EC 1.3.1.32) (Fragment).
Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.6%; Score 24; DB 1; Length 15; 36.4%; Pred. No. 1.1e+03;
                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001670; Fe-ADH.
PROSITE; PS00913; ADH_IRON_1; PARTIAL.
PROSITE; PS00060; ADH_IRON_2; PARTIAL.
Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24; DB 1; DP Pred. No. 7.4e+02; 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
Galleria mellonella (Wax moth).
                                                                                                                                                                                                                                                                                     15 AA.
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                                                                                                                                                                                                                                                                                     PRT;
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TISSUE-Larval hemolymph;
MEDLINE-98409271; PubMed-9738891;
16.6%;
66.7%;
                                                 Conservative
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                                                                                                                                                                                                                                                                                     STANDARD;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomoldea; Pentatomidae; Palomena.
                                                                                                                                                                                                                                 Score 23.5; DB 1; Length 15;
pred. No. 1.3e+03;
2; Mismatches 2; Indels
                                                                                                                                                                                           1893 MW; 23835D063B946299 CRC64;
                                                                                                                                                                          -!- INDUCTION: BY BACTERIAL INFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.2%;
50.0%;
                                                                                                                                                                                                                                   16.2%;
50.0%;
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                                                                                                                                                                                   Antibiotic; Insect immunity SEQUENCE 15 AA; 1893 MW;
                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0
المالية 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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NCBI_TaxID=55431;
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Best Local Similarity
Matches 5; Conserv
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1 VDKPDYRPRP 10
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1 VDKPDYRPRP 10
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                                                                                 TISSUE-Hemolymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Palomena prasina.
                                                                                                                                                                BACTERIA.
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P80411;
                                                                     SEQUENCE
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NEUX_HUMAN
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"The inducible antibacterial peptides of the hemipteran insect
Palomena prasina. Identification of a unique family of proline-rich
peptides and of a novel insect defensin.";
J. Insect Physiol. 42:81-89(1996).
-I- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
Wedde M., Weise C., Kopacek P., Franke P., Vilcinskas A.; "Purification and characterization of an inducible metalloprotease inhibitor from the hemolymph of greater wax moth larvae, Galleria
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Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomoidea;
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                                                                                                                                                                                      Score 24; DB 1; Length 24; Pred. No. 1.8e+03;
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                                                                                                                                                   24 24 AA; 2783 MW; 490E278E449F0C25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.2%; Score 23.5; DB 1; 50.0%; Pred. No. 1.3e+03;
                                                                                          -i- PTM: FIVE DISULFIDES BONDS ARE PRESENT.
-i- PTM: THE HEAVY CHAIN MAY BE D-GLYCOSILAFED.
-i- MASS SPECTROMETRY: WW-8350; METHOD-MALDI.
Metalloprotease inhibitor; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Palomena prasina.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                Query Match
Best Local Similarity 33.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                              1 CGEGYQSRVDHPHFP 15
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04-NOV-1995 (Rel. 32, L
15-JUL-1998 (Rel. 36, L
Metalnikowin IIA.
Palomena prasina.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pentatomidae; Palomena
                                                                                                                                                                                                                                                                    9 CEDGYARDVNGKCIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Hemolymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=55431;
                                   mellonella."
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P80409;
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P80408;
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NON_TER
SEQUENCE
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MK2A_PALPR
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                                                                                                                     Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pterygota, Neoptera, Paraneoptera, Hemiptera, Euhemiptera, Heteroptera, Panheteroptera, Pentatomomorpha, Pentatomoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          A9E3835D063B9462 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23.5; DB 1;
Pred. No. 1.4e+03;
2; Mismatches 2;
                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDX_HUMAN STANDARD; PRT; 5 AA. P04277; 20-MAR-1987 (Rel. 04, Created) 20-MAR-1987 (Rel. 04, Last sequence update)
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"Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
J. Protein Chem. 9:221-227(1990).
-!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.

IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
                                                                                                                                                                             MEDLINE=86242180; PubMed=3087352;
Mogard M.H., Kobayashi R., Chen C.F., Lee F.D., Reeve J.R. Jr., Shively J.E., Walsh J.H.;
Shively J.E., Walsh J.H.;
"The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-treated human plasma: homology with human serum albumin, neurotensin and angiotensin.";
Biochem. Biophys. Res. Commun. 136:983-988(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                              Bos taurus (Bovine), and Oryccolagus cuniculus (Rabbit). Oryccolagus cuniculus (Rabbit). Bukaryota: Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606, 9913, 9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin-potentiating peptide S5,1 (Angiotensin-converting enzyme inhibitor).
Bothrops insularis (Island jararaca) (Queimada jararaca).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serfentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                              MEDLINE-87194805; PubMed-2437111;
Carraway R.E., Mitra S.P., Cochrane D.E.;
"Structure of a biologically active neurotensin-related peptide obtained from pepsin-treated albumin(s).";
J. Biol. Chem. 262:5968-5973(1987).
-i-FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND PIR; A03239; ABHUSK.
PIR; A26693; A26693.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA; 1172 MW; C804DB4761F4140D CRC64;
014MAR-2002 (Rel. 41, Last annotation update)
Neurotensin-related peptide (NRP) (Kinetensin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 1;
Pred. No. 1e+05;
1; Mismatches (
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                                                                                                                                                                                                                                                                                                                                  SPECIES-Human, Bovine, and Rabbit;
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75.0%;
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Hypotensive agent; Venom.
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                                   Homo sapiens (Human),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                 SPECIES=Human:
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|HPYF 8
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ID BPP8_BOTIN
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SEQUENCE
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SEQUENCE
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Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
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                                                                                                                                                                                                                                                                                                                                           McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.; "Isolation and structure of a peptide toxin from the marine snail
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Gray W.R., Olivera B.M., Cruz L.J.;
"Peptide toxins from venomous Conus snails.";
Annu. Rev. Biochem. 57:665-700(1988).
-!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES,
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND
INHIBIT THEM.
                                                                                                                                                                                                                                                                                                                                                                                                            DISULFIDE BONDS.
MEDLINE=84032400; PubMed=6630187;
Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
"Conotoxin MI. Disulfide bonding and conformational states.";
J. Biol. Chem. 258:12247-12251(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY
                                                                                                                                                                                                                                                        Eukaryotā; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 14;
     Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                              1; Indels
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DEEE91898BF5E5BD CRC64;
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Pred. No. 1.4e+03;
1; Mismatches 1;
    ; DB 1;
                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                          14 AA
                                 1; Mismatches
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     Score 23;
Pred. No.
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                                                                                                                                                                                                                                                                                                                           MEDLINE=83073458; PubMed=7149738;
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60.0%;
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1499 MW;
     15.9%;
60.0%;
Query Match 15.9
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                             Conus magus (Magus cone).
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3; Conserv
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8 CGKNY 12
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091qq9 bos taurus
091x10 bos taurus
091a2 enterococcu
016350 homo sapien
094x21 enterococcu
094x12 enterococcu
09515 enterococcu
09515 atreptococc
080997 arabidopsis
061871 mus musculu
090cc5 homo sapien
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099488 porcine cir
056126 porcine cir
09647 homo sapien
Q65291 human adeno
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                                                     O9tnp5 human immun
Q16092 homo sapien
                          035905 mus musculu
                                  Ogtrf4 sus scrofa
Ogur88 aspergillus
034216 sphingomona
Q9tr98 canis famil
Q9mx47 oryzias lat
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                                                                                                                                                                                                                                                     034374 daphnia pul
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MEDLINE=96083593; PubMed=7493026;
Bonne G., Carrier L., Bercovici J., Cruaud C., Richard P., Hainque B., Bonne G., Carrier L., James M., Beckmann J., et al;
"Cardiac myosin binding protein-C gene splice acceptor site mutation is associated with familial hypertrophic cardiomyopathy.";
Nat. Genet. 11:438-440(1995).
Nat. Genet. 11:438-440(1995).
Now.TER 1 1.
SEQUENCE 22 AA; 2563 MW; 5BA92048F76774CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
CARDIAC MYOSIN BINDING PROTEIN-C (FRAGMENT).
MYBP-C.
MYBP-C.
BUKBP-C:
BUKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Q16498 h
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Pred. No. 3e+02;
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09LR42
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09WW21
09XS15
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09S1A2
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Best Local Similarity 38.9
Matches 7; Conservative
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Q1610 homo sapien
Q56610 vibrio chol
P87468 xenopus lae
Q94y92 rattus sp.
Q52918 rhizobium m
Q9450 australian
Q9p2a2 homo sapien
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Q905h2 human immun
Q90165 ascaris suu
Q9ucc0 homo sapien
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Q85496 bovine leuk
Q9ukkl homo sapien
Q9bm01 hydra litto
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69.509 Million cell updates/sec
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                                                             August 26, 2002, 10:29:34; Search time 62.22 Seconds
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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1 CGEGYQSRVDHPHFPKPIVRSITKC 25
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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of X.laevis.";
Cell 21:565-573(1980)
                                                    Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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Best Local Similarity
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9 YDLRVDPGNFP 19
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MEDLINE-95342701; PubMed=7725672;
MEDLINE-95342701; PubMed=7725672;
Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;
Kofler A., Denkins T., Serjeantson S.W., Cleve H.;
Characterization of mutants of the vitamin-D-binding protein/group
specific component: GC aborigine (1A1) from Australian aborigines and
South African blacks, and 2A9 from south Germany.";
Vox Sang. 68:50-54(1995).
EMBL; S77130; AAD14250.1;
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_raxID-666;
                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 5.1e+02;
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Pred. No. 4.8e+02;
3; Mismatches 4;
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MEDLINE=97074686; PubMed=8917113;
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EMBL; U30472; AAC44579.1; -.
NON_TER 18
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P87468;
01-MAY-1997 (TrEMBLrel. 03,
01-MAY-1997 (TrEMBLrel. 03,
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Best Local Similarity 63.5.
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01-NOV-1996 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
GC*2 PROTEIN (FRAGMENT).
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6 PKELAKLVNKC 16
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Best Local Similarity
Matches 4; Conserv
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                                                                                    NCBI_TaxID=9606;
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Q56610;
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                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-81001900; PubMed-6250724; MEDLINE-81001900; PubMed-6250724; Patient R.K., Elkington J.A., Kay R.M., Williams J.G.; Internal organization of the major adult alpha- and beta-globin genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ALPHA-GLOBIN (FRAGMENT).
Achopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gilchrist J.S., Pierce G.N.;
Tidentification and purification of a calcium-binding protein in hepatic nuclear membranes.";
J. Biol. Chem. 268:4291-4299(1993).
InterPro., IPRODISSO, Calreticulin.
PFONDSGS; calreticulin; I.
ProDom; PD001866; Calreticulin; 1.
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28.6%; Pred. No. 6.4e+02;
tive 5; Mismatches 5;
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Pred. No. 5.4e+02;
1; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heme; Oxygen transport; Respiratory protein.
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01-MAY-2000 (TrEMBLrel. 13, Last sequen
01-MUN-2001 (TrEMBLrel. 17, Last annota-
P93 CALCIUM-BINDING PROTEIN (FRAGMENT).
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54.5%;
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TISSUE=LIVER;
MEDLINE-20138537; PubMed=10672042;
Mishizawa M., Nakajima T., Yasuda K., Kanzaki H., Sasaguri Y.,
Wishizawa M., Ito S.;
"Close kinship of human 20alpha-hydroxysteroid dehydrogenase gene with
three aldo-keto reductase genes.";
Genes Cells 5:111-125(2000).
EMBL; AB037903; BAA92888.1; -.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-8119886; Pubmed-3033284;
Rice Nr., Simek S.L., Dubois G.C., Showalter, S.D., Gilden R.V.,
Stephens R.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena NCB1_TaxID=1166;
                                                                                                                                                                                                                                                                    Length 14;
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Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                       1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; Retroid viruses; Retroviridae; Deltaretrovirus NCBL_TaxID=11901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0E4C03BE93E16532 CRC64;
                                                                                                                                                                                                               SEQUENCE 14 AA; 1632 MW; 47EB1EE28D59A8D7 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last annotation update)
HYPOTHETICAL 2.6 KDA PROTEIN.
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Last annotation update)
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                                                                                                                                                                                                                                                                  Score 28; DB 4;
Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 AA.
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
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100.0%;
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                                                                                                                                                                                                                                                                  19.3%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 21 AA; 2611 MW;
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Best Local Similarity
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Best Local Similarity
                                        SEQUENCE FROM N.A.
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     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                      13 HFPKPI 18
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2 HFPVPL 7
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01-DEC-2001
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Q85496
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EMBL, APROHOGO, AAD47900.1; -. 23 23 23 23 SEQUENCE 23 AA; 2599 MW; 7B584A2225576;30 CRC64;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                                                                 MEDLINE-8529730; PubMed=2994020;
MEDLINE-85297790; PubMed=2994020;
Leong S.A., Williams P.H., Ditta G.S.;
Analysis of the 5' regulatory region of the gene for deltaminolevulinic acid synthetase of Rhizobium meliloti.";
Nuclet Catids Res. 13:5965-5976(1985).
BMBL; X02853; CAA26608.1; -.
Hypothetical protein.
SEQUENCE 20 AA; 2441 MW; BE09CF11ABCC3BB2 CRC64;
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Pred. No. 8.3e+02;
1; Mismatches 2; Indels
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Viruses; ssRNA negative-strand viruses; Moronegavirales;
Rhabdoviridae; Lyssavirus.
NCBI_TaxID-90961;
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Last annotation update)
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35.0%; Pred. No. 1.20+03;
Live 5; Mismatches 7;
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-0CT-2000 (TrEMBLrel. 15, Last ann
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57.1%;
HYPOTHETICAL 2.4 KDA PROTEIN
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Best Local Similarity
Matches 7; Conserv
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Matches 4; Conserv
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4 HFPSPFL 10
                                                                   NCBI_TaxID=382;
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Shimasaki S., Gao L., Shimonaka M., Ling N., "Isolation and molecular cloning of insulin'like growth factor-binding protein-6.";
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Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ichimura H., Parra H.-J.;
"Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in Republic of Congo-Brazzaville.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF410446; AAL10250.1;
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9826;
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                                            Length 25;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-6, IGFBP-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Endocrinol, 5:938-948(1991).
InterPro; IRR000867; IGFBP.
Bram; PF00219; IGFBP; I
SEQUENCE 25 AA; 2310 MW; 4077663151E71212 CRC64;
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19 AA; 2290 MW; 366296E191128236 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 19.3%; Score 28; DB 6; Le Best Local Similarity 57.1%; Pred. No. 1.5e+03; Matches 4; Conservative 2; Mismatches 1;
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llarity 58.3%; Pred. No. 1.4e+03;
Conservative 1; Mismatches 3;
                                          Score 28; DB 5; I
Pred. No. 1.5e+03;
3; Mismatches 4;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
                                                                                                                                                                                                                                                                                     PRT;
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                                          Query Match
19.3%;
Best Local Similarity 36.4%;
Matches 4; Conservative
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Best Local Similarity
Matches 7; Conserv
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Q905H2
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-9945376.

Poindexter K., Nelson N., DuBose R.F., Black R.A., Cerretti D.P.,

The identification of seven metalloproteinase-disintegrin (ADAM)

genes from genomic libraries.";

Gene 237:61-70(1999).

EMBL, AF158641; AAD55252.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
MARINER-LIKE TRANSPOSASE (FRAGMENT).
Hydra littoralis (swiftwater hydra).
Eukaryota, Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
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pred. No. 1.4e+03;
4; Mismatches 1; Indels
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Pred. No. 1.5e+03;
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25 25
25 AA; 2705 MW; 818B03B30EF0A19C CRC64;
                                            F85E7CBED5440B08 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
METALLOPROTEINASE-DISINTEGRIN (FRAGMENT).
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RESULT 15

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CONTEMBLE. 15, Created)

DT 01-CCT-2000 (TREMBLE. 15, Last sequence update)

ON NSARP-DELTA (FRGMRY).

ON ASAB-DELTA (FRGMRY).

ON NCBL_TAXID=6253;

RA Kato Y:

RA Kato Y:

Ascaris suum asabf-delta gene, exon 2.";

RA Kato Y:

Ascaris suum asabf-delta gene, exon 2.";

RA Kato Y:

Ascaris suum asabf-delta gene, exon 2.";

RA Kato Y:

Ascaris suum asabf-delta gene, exon 2.";

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SO SEGUENCE FROM N.A.

OUCTY MATCH

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Best Local Similarity 80.0%; Pred: No. 9.2c+02;

MATCHOS SIMILARITY 80.0%; Pred: No. 9.2c+02;

DD 2 CCTGY 6

Search completed: August 26, 2002, 10:29:35
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Copyright (c) 1993 - 2000 Compugen Ltd
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1 CGEGYQSRVDHPHFPKPIVRSITKC 25
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. 1 2 2 3 4 4 4 6 6 6 6 9 9 9 9 9 9 9 9 9 9 9 9 9	Score 145-1105 1003 1003 1003 899 688 633	% Autoh Match 100.0 73.1 72.4 71.0 71.0 71.0 71.0 71.0 71.0 71.0 71.0	Ouery e Match Length DB 5 100.0 25 21 6 72.4 25 21 72.4 25 21 3 71.0 25 21 3 71.0 25 21 9 61.4 25 21 9 61.4 25 21 8 46.9 20 18 43.4 17 21	DB 21 21 21 21 21 21 21 21 21 21 21 21 21	ID AAX80000 AAX80000 AAX79999 AAX79998 AAX91212 AAX91212 AAX6007 AAX6007 AAX50893 AAX50893	Description Optimised IgE-CH3 Optimised IgE-CH3 Optimised IgE-CH3 Modified human IgE Peptide sequence o Optimised IgE-CH3 Canine immunoglobi Antibody 15A.2 bin Antibody 15A.2 can
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New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy $\,$

Wang CY, Walfield AM; WPI; 2000-160578/14.

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                                             antigento peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, eg. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucletc acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. (conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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                                      The present invention describes immunoglobulin E (IgE)-CH3 domain
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100.0%; Pred. No. 7.2e-15;
ive 0; Mismatches 0;
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                               and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. ARY19994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
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Best Local Similarity 80.0
Matches 20; Conservative
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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding pertides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epicope (functional in genetically diverse subjects), in addition to a B cell carget epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and
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recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylatcogenic) antibodies. AAY79994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobulinulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy; disease; immunistation; anti-allergy; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
                                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                                                                                    72.4%; Score 105; DB 21; Length 25; 76.0%; Pred. No. 7.3e-09;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Optimised IgE-CH3 domain antigen peptide for human IgE.
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                                                                                                                                                                                                                                                          Pred. No. 7.36
0; Mismatches
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                                                                                                                                                                                                                                                                                                                 1 CGEGYQSRVDHPHFPKPIVRSITKC 25
                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 21; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunization against allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY79998 standard; Peptide; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNBI-) UNITED BIOMEDICAL INC.
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                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                      Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                            25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY79998;
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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maximize cross-reactivity to the natural target. They induce safe

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigon; HBV; immunopenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoploblin E; IgE; anti-allergic; Plasmodium falciparum; circumsporozoite; antimalarial; CEPP; cholesteryl ester transport protein; anti-arteriosclerotic.
(non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunotherapy; for inhibition of the action of luteinising hormone releasing hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration); for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target
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                                                                                                                    Length 25;
                                                                                                                                                        Indels
                                                                                                                  Score 103; DB 21;
Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified human IgE CH3 domain, SEQ ID NO:92.
                                                                                                                                                      3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or human immune deficiency virus
                                                                                                                                                                                                                                                                                                                              AAY91212 standard; peptide; 25
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                                                                                                                71.0%;
68.0%;
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                                                                                                                                Local Similarity 68.0 nes 17; Conservative
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                                                            Sequence
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                    AAY91212;
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Matches
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Wang CY;

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antigen. The day replace cariner proteins and pathogen-derived Theiper epitopes. Sequence AAY91121 represents a promiscuous Theiper epitope from the measles virus F (MVF) protein and sequences AAY91122-Y91146.

AAY91225 and AAY91143 represents a promiscuous Thepitope based on the MAY91256 and AAY91143 represents a promiscuous Thepitope based on the MAY91155 are synthetic epitopes derived from this HBV epitope. AAY91156 are synthetic epitopes derived from this HBV epitope. AAY91156-Y91196, AAY91127 and AAY9124-Y91244 are antigenic peptides. Comprising an LHRH sequence Joined to a promiscuous The epitope. AAY91197 is the LHRH target antigenic peptides comprising somatostatin, and AAY91201-Y91207 are antigenic peptides comprising somatostatin, and AAY91201-Y9120 PY90211 are WH The epitope/CDA CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AAY90212 is a modified version of a human IgE chantigenic peptides which may be used to the treatment of allergies.

AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) contingenic peptides which may be used in the treatment of allergies.

AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) contingen, and AAY91221-Y91222 comprise this peptide and a Th epitope and may be used in a malaria vaccine. AAY9128-Y91231 represent corprived peptides and AAY9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-Y9123-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             luteinising hormone-releasing hormone; spermatogenesis; ovulation; osstrus; sexual development; sex hormone; promiscuous T helper epitope; vaccine; contraceptive; hormone-dependent tumour; prostate cancer; breast cancer; endometriosis; boar taint; meat quality; immunocastration.
  antigen. Th can replace carrier proteins and pathogen-derived T helper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 1.5e-08;
"..matches 5; Indels
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68.0%;
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Best Local Similarity
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                                                                                                                                                                                 The specification describes peptide immunogens comprising a synthetic helper T cell (Th) epitope and a target antigen, luteinising hormone-releasing hormone (LHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, oestrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast, also endometriosis); to prevent boar taint (and improve meat guality) and for immunocastration. The present sequence appears in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                    hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                  New peptide immunogen containing luteinising hormone-releasing horn
antigen site and helper T cell epitope, for e.g. contraception and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 103; DB 21; Length 25;
Pred. No. 1.5e-08;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Optimised IgE-CH3 domain antigen peptide for horse IgE.
                                                                                                                                                     Disclosure; Page 92; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
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68.0%;
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                                                WPI; 2000-160562/14.
                                                                                                                    cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Equus caballus.
                                                                                                    antigen site
treatment of
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Length 20;

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Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                          AAY50893;
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                                                                                                                                                                                                 AAY50893
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                                                    antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the spilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding petides or in DNA vaccines. (conjugates of (I) that include a promiscuous Thelper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural conformational features and maximize cross-reactivity to the natural conformational features and conformation anaphylactogenic) antibodies. AAY7994 to AAY80084 represent anino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW24098-106 are peptide fragments containing at least 5 continuous amino acids of the partial canine immunoglobulin E (IgE) protein shown in AAW24097. The peptides are used for the preparation of anti-canine IgE antibody. The anti-canine IgE antibody can be used for the diagnosis of canine allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                        The present invention describes immunoglobulin E (IgE)-CH3 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine immunoglobulin E peptide fragment and related DNA - useful for the preparation of anti-canine immunog.cobulin E antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 89; DB 21; Length 20.
Pred. No. 1.8e:-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
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  Claim 1; Page 146; 155pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canine immunoglobin E peptide 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.4%;
60.0%;
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Best Local Similarity 60.0°
Matches 15; Conservative
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ANY50876-Y50900 represent peptide mimotopes used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                  Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or prophylaxis of canine allergy
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                                                4; Indels
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  Score 68; DB 18;
Pred. No. 0.0021;
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Pred. No. 0.0097;
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80.08;
46.9%;
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99US-0281760
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                                                                                         RVDHPHFPKPIVRSITK 24
                                                                                                                  Conservative
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mermer B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || ||| || || ||||||| 3 rvthphlpkdivrsi
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94US-0178583
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                                                                           Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IgE peptide antagonist.
                                       (GETH ) GENENTECH INC.
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                                                                                                             WPI; 1999-579941/49
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Best Local Similarity
Matches 10; Conserv
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allergic disease.
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07-JAN-1994;
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                                                                           Jardieu PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound igE, and which doesn't bind to igE when the igE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound igE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.
                                                   Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Binding proteins used for treatment or prophylaxis of canine allergy -
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receptor-binding; binding determinant sequence; anti-IgE antibody;
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               Antibody 15A.2 canine IgE binding epitope 1.
                                                                                                                                                                                                                                                                                                                                                                  Mermer B, Francoeur G;
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                                                                                                                                                                                                                               99EP-0107035
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99US-0281760
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les 12; Conserv
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30-MAR-1999;
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                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                  Lawton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Invention
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Matches
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Immunoglobulin E variants as peptide antagonists useful for raising and screening anti-immunoglobulin E (IGE) antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment of allergic
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receptor-binding; binding determinant sequence; anti-IgE antibody;
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55.6%;
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17 AA;

Sequence

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                                                             The invention provides immunoglobulin E (Igl;) antagonists comprising one
                                                                          or more of the PoepsilonRI receptor binding determinant sites of human igs. The antagonists include 1gs variants comprising an immunoglobulin template and binding determinant sequences :bds) CDBGA. BFbGAs and the sequence shown in AAY42581. The CDBGAS (CD loop binding determinant sequence) are selected from the sequences shown in AAY42577 and the FBPGA (FB loop binding determinant sequence) are selected from sequences shown in AAY4278-442580. The variants are useful in raising and screening anti-IgE antibodies, in the isolation and purification of PrepsilonRI receptor and in the treatment and prophylaxis of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound ige, and which doesn't bind to ige when the ige is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound ige molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.

ANYSORYC YSOUO represent peptide mimotopes: used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
epitope; prophylaxis; treatment; mimotope.
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Pred. No. 0.02;
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                                Disclosure; Column 9; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY50896 standard; peptide; 17
                                                                                                                                                                                                                                                                                                            42.8%;
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99US-0281760
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Best Local Similarity
Matches 10; Conserv
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ANX50876-X50900 represent peptide mimotopes used in the method of the
                                                                                                                                                                                                                                                    Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
                           Gaps
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 DB 21; Length 17; 0.055;
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                           4; Indels
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Pred. No. 0.15;
3; Mismatches
Score 58; DB 2
Pred. No. 0.055
2; Mismatches
                                                                                                                                                                                                                              Antibody 15A.2 human IgE binding epitope 1.
                                                                                                                                             AAY50895 standard; peptide; 17 AA.
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 40.0%;
62.5%;
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56.2%;
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Query Match 40.0
Best Local Similarity 62.5
Matches 10; Conservative
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| qcrvthphlpralmrs 16
                                                     6 QSRVDHPHFPKPIVRS 21
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Best Local Similarity
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30-MAR-1999;
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This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.
                                                                                  Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
epitope; prophylaxis; treatment; mimotope.
                                                                                                                                                                                                                                                                                                                                                                          Binding proteins used for treatment or prophylaxis of canine allergy
                                                    Antibody 15A.2 swine IgE binding epitope 1.
                                                                                                                                                                                                                                                                                                                   Mermer B, Francoeur G;
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                                                                                                                                                                                                                 99EP-0107035,
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99US-0281760
                         24-FEB-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 AA;
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30-MAR-1999;
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                                                                                                                                                                                                                                                                                                                   Lawton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
                                                                                                                            Synthetic.
AAY50898;
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Gaps ; 0 Ouery Match 37.2%; Score 54; DB 21; Length 17; Best Local Similarity 71.4%; Pred. No. 0.22; Matches 10; Conservative 1; Mismatches 3; Indels

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Search completed: August 26, 2002, 10:18:42 Job time: 698 sec

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68.0%; Pred. No. 1.7e-09;
iive 3; Mismatches 5;
US-08-395-602A-1
US-08-0116-733-12
US-08-165-59
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US-08-466-76-9
US-08-986-6598-8
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US-08-650-915A-61
US-07-801-812A-8
US-08-433-318A-86
US-08-433-318A-86
US-08-433-318A-86
US-08-433-318A-86
US-08-313-686-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 4.24
ATTORNEY AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-754-6849
INFORMATION FOR ESQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 95, Application US/09100414B Patent No. 6025468
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
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Best Local Similarity 68.0
Matches 17; Conservative
      ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-09-100-414B-95
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US-09-100-414B-95
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Sequence 518, Appl
Sequence 218, Appl
Sequence 371, App
Sequence 5, Appl 1
Sequence 10, Appl
Sequence 398, Appl
Sequence 399, Appl
Sequence 298, Appl
Sequence 7, Appl 1
Sequence 12, Appl 1
Sequence 222, Appl 2
Sequence 222, Appl 3
Sequence 222, Appl 3
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Sequence 19, Appl
Sequence 7, Appl
Sequence 7, Appli
Sequence 7, Appli
Patent No. 5177197
                                                                                                                                             August 26, 2002, 10:19:36; Search time 33.13 Seconds (without alignments) 18.432 Million cell updates/sec
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US-08-232-539D-20
US-08-630-645-7
                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-630-645-81
PCT-US96-10220-8
US-08-447-010-3.4
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5177197-5
                                                                                                                                                                                                                                                                                CGEGYQSRVDHPHFPKPIVRSITKC 25
                                                                                                                                                                                                                                                                                                                                                                                            231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_AA:*
                                                                                                                                                                                                                              US-09-701-623C-7
                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
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No.
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Pred. No. 0.0031;
3; Mismatches 5; Indels
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CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: WinPatin (concurred CURRENT APPLICATION DATA:

PAPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
FILING DATE: 14-AuG-1991
ATTORNEY/AGRAT INFORMATION:
NAME: SVODOGA, Craig G
REGISTRATION NUMBER: 39,044
RESTRANTON NUMBER: 99,044
FILEFRAN GOOGA, Craig G
REGISTRATION NUMBER: 99,1893
FILEFRAN GOOGA, Craig G
REGISTRATION NUMBER: 99,1893
FILEFRAN GOOGA, CASSO ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: Amino Acid
CS-08-232-539D-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: LDFF COMPUTER: OPERATING SYSTEM: PC-DOS/FN3 CONTROL WINPALIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILLING DATE: 21-Apr-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GEGYQSRVDHPHFPKPIV 19
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Best Local Similarity 55.6
Matches 10; Conservative
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71.0%; Score 103; DB 4; Length 25;
Best Local Similarity 68.0%; Pred, No. 1.7e-09;
Matches 17; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94080
COMPUTER READABLE FORM:
WEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      Sequence 95, Application US/09303323
Patent No. 6228987
GENERAL INPORMATION:
APPLICANT: Wang, Chang Xi
TITLE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-232-539D-19
Sequence 19, Application US/08232539D
Sequence 19, Application US/08232539D
GENERAL INFORMATION:
APPLICANT: Dresta, Leonard G.
APPLICANT: Jardiau, Paula M.
TITLE OF INVENTION: 1gE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIEFCATION:
PRIOR APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NUMBER: MATER H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGEGYQSRVDHPHFPKPIVRSITKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-/51-00.
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-09-303-323-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                      US-09-303-323-95
                                                                                                                                                                                                                         CITY:
STATE:
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Gaps

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PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESUL.
5177197-5
; RAPLICANT: KANZAKI, TETSUTO:OLOFSSON, ANDERS; MOREN, ANITA;
; RAPLICANT: KANZAKI, TETSUTO:OLOFSSON, ANDERS; MOREN, ANITA;
; WENSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,
; LENA; HELDIN, CARL-HENRIK
; HUMAN TRANSFORMING GROWTH FACTOR-BETAI-BINDING PROTEIN
NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                               COMPUTER TEACHBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10220
FILING DATE:
                                                                                                             TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DIS
TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AM
NUMBER OF SEQUENCES:
ADDRESSE: ADDRESS:
ADDRESSE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                        Sequence 7, Application PC/TUS9610220
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
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66.7%;
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Best Local Similarity 66./v,
8; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 amino acids
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D.C.
USA
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PCT-US96-10220-7
                                                                                                                                                                                                                                                                                                              20004
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5177197-5
                                          PCT-US96-10220-7
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, BLISS
APPLICANT: FRANGIONE, BLISS
TITLE OF INVENTION: THEREOF FOR TREATMENT JF DISORDERS OR DISBASES ASSOCIATED
TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
TORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
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Pred. No. 0.0034;
3; Mismatches 5; Indels
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Pred. No. 14;
0; Mismatches 4; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/630,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRNE: 202-628-5197
TELEFRX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08630645
Patent No. 5948763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        42.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.5%;
                                                                                                                                                                                                                                   2 GEGYQSRVDHPHFPKPIV 19
                                                                                                                                                                                                                                                            7 GETYQCRVTHPHLPRALM 24
                SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: Amino Acid
                                                                                                                                                        Query Match 42.89
Best Local Similarity 55.65
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.5
Best Local Similarity 66.7
Matches 8; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 SRVDHPHFPKPI 18
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                                                                         ; TOPOLOGY: Linear
US-08-232-539D-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds.
D.C.
USA
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COUNTRY:
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Sequence 218, Application US/09258754
; Sequence 218, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Rucslahti, Erkki
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER FILING DATE: 1999-03-13
; NUMBER OF SEQ 1D NOS: 452
; SOFFWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
TITLE OF INVENTION: DIPTHERIA TOXIM EPITOPES
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 2; Length 20; Pred. No. 40;
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                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/564,972
FILING DATE: 30-NOV-1995
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600.344US1
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPHONE: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.18;
75.08;
                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
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3 GYQKTVDH 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-564-972-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GYQSRVDH 11
                                                                                                                                                                                   COUNTRY:
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LENGTH: 13
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Patent No. 5843462
GENERAL INFORMATION:
TITLE OF INVENTION: DIPTHERIA TOXIM EPITOPES
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
                                                                Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
40;
                                                            Score 35; DB 6;
Pred. No. 25;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,972
FILING DATE: 30-NOV-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 55, Application US/08564972; Patent No. 5843462; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: WOESSIGE, WAITEN D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 600.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
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75.0%;
                                                            Query Match 24.1%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.07
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: 1
ORIGINAL SOURCE:
US-08-564-972-54
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13 GYQKTVDH 20
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                                                                                                                              1 CGEGYQ 6
                                                                                                                                                              3 CGQGYQ 8
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ZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Minr
STATE: MN
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US-08-564-972-55
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US-08-602-999A-371
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TOPOLOGY:
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                                                                                                                                                            Gaps
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APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
FILE REFERENCE: P-LJ 2892
CURRENT APPLICATION NUMBER: US/09/042,107
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 436
SOFTWARE: Patentin Ver. 2.0
                                  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-258-754-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DOULLIAM, Lawrence A.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
                                                                                                                     4; Length 13;
                                                                                                                                                          1; Indels
                                                                                                              Score 34; DB 4
Pred. No. 36;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 371, Application US/08602999A Patent No. 6184205 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                Sequence 218, Application US/09042107 Patent No. 6232287 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SPARKS, Andrew B
ORGANISM: Artificial Sequence
                                                                                            Query Match
Best Local Similarity 62.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.4
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || |||::
1 CGPGYQAQ 8
                                                                                                                                                                                            1 CGEGYQSR 8
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Gaps
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METHOD FOR DETECTION OF HUMAN PAPILLOMAVIRUS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/678,974D
FILING DATE: 25-JUN-1991
CLASSIFICATION: 435
ATTONEY/AGENT TITE:
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 4
Pred. No. 51;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
TITLE OF INVENTION: METHOD FOR DETECTION (
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
STREET: 1730 RHODE ISLAND AVENUE, N.W.,
                             UMBER: US/08/602,999A
16-FEB-1996
                                                                                                                                                   REFERENCE/DOCKET NUMBER: 1011-
TELECOMMUNICATION INFORMATION:
TELEPRONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 371:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application US/07678974D
; Patent No. 5629146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNET/AGENT INFORMATION:
NAME: ALSENBERG, Irwin M.
REGISTRATION NUMBER: 19,007
REFERENCE/DOCKET NUMBER: SG
TELECOMMUNICATION INFORMATION:
                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Lealle
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.4%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 20036-3186
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                            FILING DATE:
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1 HPHAPPP 7
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                                                                                    Gaps
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US-08-945-168-10
Sequence 10, Application US/08945168
Sequence 10. Application US/08945168
Sequence 10. Sequence 11. Sequence
                                                                                5;
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Score 34; DB 1; Length 20;
Pred. No. 57;
1; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Belease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,168
FILING DATE: 18-DEC-1997
CLLASSIFICATION: DATA:
APPLICATION NUMBER: PCT/SE96/00533
PRIOR APPLICATION NUMBER: PCT/SE96/00533
PRIOR APPLICATION NUMBER: B 9501512-9
FILING DATE: 24-APR-1995
PRIOR APPLICATION NUMBER: SE 9501512-9
FILING DATE: A4-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F:
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 7752-0002-0 PCT
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.4%; Score 34; DB 2;
63.6%; Pred. No. 57;
iive 1; Mismatches
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Parent No. 6184205
Parent Northwarton:
APPLICANT: SPARKS, Andrew B.
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INFORMATION FOR SEQ ID NO: 10:
23.4%;
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LENGTH: 20 amino acids
                                    Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    703-413-2220
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Matches 7; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                    9 VDHPHFP--KP 17
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10 VGHPYFPIKKP 20
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COUNTRY: US
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-602-999A-398
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Query Match
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                                           APPLICANT: DER, CNBLULLE,
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 4; Length 17; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: August 26, 2002, 10:19:37 Job time: 393 sec
KAY, Brian K.
THORN, Judith M.
QUILLIAM, Lawrence A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.8%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4'
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELERAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-602-999A-398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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4 HPNFQKP 10
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Sequence 2 Sequence 1 Sequence 3 Sequence 3 Sequence 5 Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 1 Sequence 1 Sequence 1

Sequence 1, A Sequence 12, Sequence 11, Sequence 11,

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database :

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Length 25;
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Pred. No. 1.1e-16;
Mismatches 0;
PCT-US96-09319-29
US-08-317-310A-15
DCT-US95-13041-15
US-08-477-650-37
US-08-191-866D-59
US-08-108-949B-59
US-08-185-949B-59
US-09-047-125-31
US-09-047-125-31
US-08-150-203A-10
US-08-150-203A-10
US-08-150-203A-10
US-08-150-203A-10
US-08-147-404-1
US-08-147-404-1
US-08-147-404-1
US-08-1890-719-12
US-08-890-719-13
US-08-890-719-13
US-08-890-719-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INPORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEFRAE: 212-758 4800
TELEFRAE: 212-751-6849
INFORMATION FOR SEQ ID NO: 95:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 95, Application US/09100414B Patent No. 6025468 GENERAL TINFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
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Best Local Similarity 100.0%; P
Matches 25; Conservative 0;
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LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
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MOLECULE TYPE: peptide
US-09-100-414B-95
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     RESULT
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                                                                                                                                                                             August 26, 2002, 10:03:14; Search time 34.18 Seconds
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/cgn2_6/ptodata/2/iaa/6A_COIB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COIB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
                                                        Compugen Ltd
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US-09-100-414B-98
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US-09-303-323-100
US-09-100-414B-101
US-09-100-414B-95
US-09-303-323-101
US-09-303-323-95
US-09-303-323-95
US-09-303-323-59
US-08-36-5599-56
US-08-36-5399-56
US-08-36-5399-19
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                             GenCore version 4.5
Copyright (c) 1993 - 2000 Com
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Maximum DB seq length: 2000000000
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100.0%; Pred. No. 2.1e-16;
tive 0; Mismatches 0;
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Pred. No. 2.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 99, Application US/09100414B
Fatent No. 6025468
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAIJA H. LID
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INPORMATION:
TELEPHONE: 212-754-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CRARACTERISTICS:
LENGTH: 42 and no acids

WINDER: AMIDO ACIDS
SEQUENCE CRARACTERISTICS:
LENGTH: 42 and no acids
             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEYAGENT INPORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
                                                                                                                                                                1151-4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGETYQSRVTHPHLPRALMRSTTKC 25
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                                                                                                                                                          REFERENCE/DOCKET NUMBER: 1151
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-758-6849
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acids
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100.0%;
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Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-98
Word 97
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Best Local Similarity
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US-09-100-414B-99
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SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-00-100-414B-98
Sequence 98, Application US/09100414B
Sequence 98, Application US/09100414B
PALENT NO.26024686.25
GENERAL TINFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                       GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSE: MOTGAN & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                          SCETWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPHONE: 212-751-6849
INFORMATION FOR SEQ ID NO: 95:
                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                    Sequence 95, Application US/09303323
Patent No. 6228987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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US-09-303-323-99
US-09-303-323-99; Application US/09303323
Eatent No. 6228987
GENERAL INFORMATION:
TAPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNGENS
TITLE OF INVENTION: IMMUNGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
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TELEPHONE: 212-758-4800
TELEPAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: 1 DER FO COMPUTER: CONTROL SOFTWARE: Word 97 CURRENT APPLICATION DATA: BAPLICATION NUMBER: US/09/303,323 FILING DATE: 30-APR-1999
                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-41:
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-758 4800
TELEFRAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGETYQSRVTHPHLPRALMRSTTKC
                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 98:
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                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 42 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: peptide US-09-303-323-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                FILING DATE: 3 CLASSIFICATION:
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Pred. No. 2.1e-16;
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US-09-303-323-98
Sequence 98, Application US/09303323
Patent No $$ 56228987^{\psi}$; Fatent No $$ 56228987^{\psi}$; Fatent No $$ 56228987^{\psi}$; Fatent No $$ 5628987^{\psi}$; TITLE OF INVENTION: NOVEL LHRH PEPTIDE; TITLE OF INVENTION: NOWNINGENS: NOWNINGENS: NOWNINGENS: ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York STATE: NY
COUNTRY: USA
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                       APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
                                                                                                                                              US-09-100-4148-100

Sequence 100, Application US/09100414B

Patent No. 6025468

GENERAL INFORMATION:
                                       1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                           18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGETYQSRVTHPHLPRALMRSTTKC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPHONE: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; S. Best Local Similarity 100.0%; P. Matches 25; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 100: SEQUENCE CHARACTERISTICS: LENGTH: 4.2 amino acids TYPE: amino acid
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-09-100-414B-100
                                                                                                                                                                                                                                                                                                                                                             linear
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Matches
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0; Gaps

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Length 45;
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Pred. No. 2.3e-16;
Mismatches 0;
               GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1151-4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/303,323
FILING DATE: 30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 101, Application US/09303323 Patent No. 6228987
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STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Scc
100.0%; Pr
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NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFRENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                               ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-09-100-414B-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCT: 45 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-09-303-323-101
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                                                                                                                                                                           CITY: N
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0
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                                                                                                                                                           Length 42;
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                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 140; DB 4; Best Local Similarity 100.0%; Pred. No. 2.1e-16; Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            Sequence 100, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNOCENS
TITLE OF INVENTION: IMMUNOCENS
TITLE OF ENCENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAILSH H. LIN
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM:
POPERATING SYSTEM:
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESUL* 9
US-09-100-414B-101
; Sequence 101, Application US/09100414B
                                                                                                                                                                                                                                   1 CGETYQSRVTHPHLPRALMRSTTKC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 100:
                 : 42 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
SEQUENCE CHARACTERISTICS
LENGTH: 42 amino acids
                                                                         ; MOLECULE TYPE: peptide US-09-303-323-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-09-303-323-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
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                                       TYPE: ami
TOPOLOGY:
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Length 46;
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100.0%; Score 140; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.3e-16;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                       Sequence 97, Application US/09100414B
Patent No. 6025468
GENERL INFORMATION:
GENERL INFORMATION:
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
TITLE OF INVENTION: IMMUNOGENS
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTGAN & Finnegan, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 95, Application US/09303323
Fatent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                           ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 CGETYQSRVTHPHLPRALMRSTTKC 46
    22 CGETYQSRVTHPHLPRALMRSTTKC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPHONE: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                           CIP: 1015.4-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 46 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-09-100-414B-97
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                                                                                    RESULT 12
US-09-100-414B-97
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                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                              Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 140; DB 4;
100.0%; Pred. No. :38-16;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 96, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: FC WILLIOUS SOFTWARE: WOR'D 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-UUNE-1998
CLASSIFICATION: 4.24
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-754-4800
TELEFAN: 212-751-6849
: INFORMATION FOR SED ID NO: 96:
SEQUENCE CHARACTERISTICS:
                                                                                                        1151-4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/100,414 FILING DATE: 20-JUNE-1998 ATTORNEY/AGENT INFORMATION:
                                                                              REGISTRATION NUMBER: 29,323
REFREENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                             LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.C
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-09-303-323-101
                                                                 Maria H. Lin
                                                                                                                                                                                                                                                                          linear
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Best Local Similarity
Matches 25; Conserv
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1 CGETYQSRVTHPHLPRALMRSTTKC 25

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                                                                                                         Length 46;
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                                                                                                                                                 Indels
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                                                                                                      100.0%; Score 140; DB 4;
100.0%; Pred. No. 2.3e-16;
ive 0; Mismatches 0;
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Pred. No. 3.4e-16;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: NY
COUNTRY: USA
2 IP: 10154-0054
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION NUMBER: 29,323
REGISTRATION NUMBER: 29,323
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEFONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 102:
                                                                                                                                                                                                                                                                                                                        Sequence 102, Application US/09100414B
Fatent No. 6025468
GENERAL INFORMATION:
APPLICANT: WANG, Chang YI
TITLE OF INVENTION: INMUNOGENS
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: August 26, 2002, 10:05:18 Job time: 124 sec
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Best Local Similarity 100.0%; P
Matches 25; Conservative 0;
                                                                                                      Query Match
Best Local Similarity 100.0
Matches 25; Conservative
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LENGTH: 63 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                     ; MOLECULE TYPE: peptide US-09-303-323-97
  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                             RESULT 15
US-09-100-414B-102
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                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INPORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFERRICE/POCKET NUMBER: 151-4157
TELECOMMUNICATION INPORMATION:
TELECPHONE: 212-758-4800
TELEPHONE: 212-758-4800
TELEPHONE: 212-758-4800
TELEFRA: 212-751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 97, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: IMMUNGENS
NUMBER OF ENVENTION: IMMUNGENS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1151-4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. Lin
RAFETSFRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 CGETYQSRVTHPHLPRALMRSTTKC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
OPERATING SYSTEM: PC Windows SOFTWARE: Word 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 97:
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                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-96
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us-09-701-623c-5.closed.rai

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: FLOPPy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY AACHT INFORMATION:
NAME: MAINE H. Lin REGISTRATION NUMBER: 29,323
REFREENCE/DOCKER NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEPHONE: 212-758-4800
TELEPHONE: 212-758-4800
TELEPHONE: 212-751-6849
INFORMATION FOR SEG ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGETYQSRVTHPHLPRALMRSTTKC 25
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100.0%; Pr
tive 0;
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Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10154-0054
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                                                                                                                                               August 26, 2002, 10:13:04; Seirch time 33.13 Seconds (vithout alignments)
18.432 Million cell updates/sec
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17, Appl
9, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/iaa/5A_CONB.pep:*
/cgn2_6/ptodata/2/iaa/5B_CONB.pep:*
/cgn2_6/ptodata/2/iaa/6A_CONB.pep:*
/cgn2_6/ptodata/2/iaa/6B_CONB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_CONB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_CONB.pep:*
GenCore version 4..5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-232-539D-19

US-08-232-539D-20

US-07-976-358-15

US-07-976-358-15

US-07-976-358-11

US-07-976-358-11

US-07-976-358-11

US-07-976-358-11

US-08-017-258-11

US-08-017-278-14

US-08-011-3078-9

US-08-111-3078-9

US-08-011-3078-9

US-08-011-3078-9
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    CGETYQSRVTHPHLPRALMRSTTKC 25

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                                                                                                         protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
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Maximum DB
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Gaps

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Length 25; Indels

Score 140; DB 3; Pred. No. 1.1e-16; Mismatches 0;

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Sequence 35, Appl
Sequence 27, Appl
Sequence 32, Appl
Sequence 31, Appl
Sequence 313, App
Sequence 313, App
Sequence 160, App
Sequence 160, App
Sequence 160, App
Sequence 17, Appl
Sequence 371, Appl
Sequence 9, Appli
                                                                                                                                                                         Sequence
US-08-195-006-35
PCT-US94-07644A-27
PCT-US94-07644A-35
US-08-136-82
US-08-146-80-3
US-08-617-159B-313
US-08-617-159B-313
US-08-617-159B-160
PCT-US96-08909-160
US-08-662-999A-371
PCT-US92-07813-7
US-08-466-615-9
US-08-466-615-9
US-08-440-861-37
US-08-440-861-37
US-08-440-861-37
US-08-440-861-37
US-08-440-861-37
US-08-440-861-37
US-08-440-861-37
US-08-440-861-37
                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                         US-09-100-414B-95
Sequence 95, Application US/09100414B
Fatent Now 60055468*
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
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Pred. No. 5.5e-09;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compactible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINDALIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07-JAN-1994
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
      21-Apr-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardicu, Paula M.
TITLE OF INVENTION: 19E Antagonists
NUMBER OF SEQUENCES: 60
NUMBER OF SEQUENCES: ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                      P0718P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE-FOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
                             APPLICATION DATE:
CLASSIFICATION NUMBER:
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRICHA APPLICATION DATE:
APPLICATION NUMBER: 08/178583
FILING DATE: 07.-JAN-1994
PRICHA APPLICATION DATE:
APPLICATION NUMBER: 07/744768
FILING DATE: 14 ANG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SVODOGA, CTA19
WinPatin (Genentech)
                                                                                                                                                                                                                                                    NAME: SVODCA, CTAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 90716
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPHONE: 650/25-9881
INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-232-539D-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 GETYQCRVTHPHLPRALM 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GETYQSRVTHPHLPRALM 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
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US-08-232-539D-20
SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                 Sequence 95, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTGAN & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-122-539D-19

Sequence 19, Application US/08232539D

Patent No. 5965709

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVERTION: IGE Antagonists

MUNBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA WAY

CITY: South San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                            CONTEXT: USA

ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1151-4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-41!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-756-4800
TELEPAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 25 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : MOLECULE TYPE: peptide US-09-303-323-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 30 CLASSIFICATION:
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             US-09-303-323-95
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Gaps

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Sequence 18, Application US/07976358
Patent No. 5445932
GENERAL INFORMATION:
APPLICANT: FIELDS, Howard A.
APPLICANT: KHUDYAKOV, Yuri
APPLICANT: FAVOROV, Michael
TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                         APPLICANT: FAVOROV, Michael
TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
NUMBER OF SEQUENCE: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC COMPATIBLE
COMPUTER: DE PC FOS MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/976,358
FILING DATE: 19921117
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington, D.C.
COUWTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 1
Pred. No. 24;
2; Mismatches
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STREET: 3000 K Street, N.W., Suite 500
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FILING DATE: 19921117
                             Howard A.
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50.0%;
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(202)672-5399
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 25 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.0
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                 Washington, D.C.
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                                                      KHUDYAKOV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 YSSQPTLPSLPRVV 21
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US-07-976-358-15
                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20007-5109
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                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FIELDS, Howard A.
APPLICANT: KHUDYAKOV, Yuri
APPLICANT: KHUDYAKOV, Yuri
APPLICANT: FAVOROV, Michael
TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                   Score 93; DE 2; Length 24; Pred. No. 6.1e-09;
                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/976,358
FILING DATE: 19921117
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٠.
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Pred. No. 23;
2; Mismatches
                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/07976358
Patent No. 5445932
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/07976358 Patent No. 5445932 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Foley & Lardner
                             20:
                                                                                                                                                                                                                                      66.48;
94.48;
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50.0%;
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: Amino Acid
TYPE: Linear
                                                                                                                                                                                                                                                                                                                                       2 GETYQSRVTHPHLPRALM 19
                                                                                                                                                                                                                                                                                                                                                                       7 GETYQCRVTHPHLPRALM 24
                                                                                                                                                                                                                                Query Match 66.49
Best Local Similarity 94.49
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 amino acids
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Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-07-976-358-24
                                                                                                                            ; TOPOLOGY:
US-08-232-539D-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-976-358-15
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US-07-976-358-24
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Gaps ö

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APPLICANT: FIELDS, Howard A.
APPLICANT: KHUDYAKOV, Yuri
APPLICANT: FAVOOV, Michael
TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
CORRESPONDENCE 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Marsden, Howard S
TITLE OF INVENTION: PREPTIDE STRUCTURES AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5963357th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA
2IP: 22201.4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: STATEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/976,358
FILING DATE: 19921117
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
RECISTRATION NUMBER: 29,768
RECISTRATION NUMBER: 29,768
TELEPHONE: (202)672-5300
TELEPRA: (202)672-5300
TELEPRA: (202)672-5300
TELERA: 904136
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 1;
Pred. No. 35;
2; Mismatches
                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                          Sequence 17, Application US/07976358 Patent No. 5445932 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09017205 Patent No. 5965357
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 YOSRVTHPHLPRAL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 YSSOPTLPPLPRVV 21
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US-07-976-358-17
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US-09-017-205-9
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Sequence 21, Application US/07976358
Patent No. 5445932
GENERAL INFORMATION:
APPLICANT: FIELDS, Howard A.
APPLICANT: FAVOROV, WITH
TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLGY & Lardner
STREET: 3000 K Street, N.W., Suite 500
COLTY: Washington, D.C.
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Pred. No. 24;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                              Length 25;
                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE PATENTING STATES OF THE SOFTWARE PATENT RELEASE #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/976,358 FILING DATE: 19921117 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/134 NIHD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              DB 1;
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/134 NIHD
RELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
TELERA: (202)672-5399
TELERA: (202)672-5399
TELERA: (202)672-5399
TELERA: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                              Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 21:
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50.0%;
                                                                                                                                                                                                                                                                                                                                              25.0%;
                                                                                                                                                                                                            : 25 amino acids
AMINO ACID
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                  5 YOSRVTHPHLPRALMRS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 YSSHPILPFLPRAVVPS 24
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 47.1 Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.0
Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-07-976-358-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-976-358-21
                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                              Query Match
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                23.2%;
53.8%;
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              Modified-site
                                                                                                                                                                Query Match 23.2
Best Local Similarity 53.8
Matches 7; Conservative
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Best Local Similarity 42.9
Matches 6; Conservative
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internal
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ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
          : NAME/KEY: Modified-e

: LOCATION: 4..6

: OTHER INFORMATION: ,

: OTHER INFORMATION: n

: OTHER INFORMATION: n

: OTHER INFORMATION: n
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1 GDTHRGHLRH-HLP 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
FRAGMENT TYPE:
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Pred. No. 35;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Talmadge, James E.
TITLE OF INVENTION: Anti-inflammatory Pol/Peptide
TITLE OF INVENTION: Antagonists of Human interleukin-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTY: USA
ZIP: 19103-230

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARRE: Patentin Release #1.0, Versior, #1.30
CURRENT APPLICATION DATA:
        SÕFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide from HSV-2 glycoprotein G; FRAGMENT TYPE: internal US-09-017-205-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/671,094B
FILING DATE: 28-JUN-1996
CLASSIFICATION: 514
                                            APPLICATION NUMBER: US/09/017,205
FILING DATE: 02-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08671094B Patent No. 5912232
                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 6308(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)563-4100
TELEFAX: (215)563-404
INFORMATION FOR SED NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    23.6%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.6
Best Local Similarity 53.6
Matches 7; Conservative
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 TYAARVTYYRLTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 TYQSRVTHPHLPR 16
                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
SOFTWARE:
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/note= "The cysteine residues
may be substituted with aminobutyric acid, homocysteine or
diaminosuberic acid."
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/08077797A
Patent No. 5679548
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Rosenblum, Jonathan
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL
TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                       Score 32.5; DB 2; Length 15;
Pred. No. 34;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
STREET: 10666 No. 5679548th Torrey Pines Road, TPC8
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/077,797A

FILING DATE: U-JUN-1993

CLASSIFICATION 1435

PRIOR APPLICATION 1435

PRIOR APPLICATION NUMBER: US/08/012,566

FILING DATE: 02-FEB-1993

ATFORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REGISTRATION NUMBER: 34,163

REGISTRATION NUMBER: 34,163

RELEPHONE: 619-554-2937

TELEPHONE: 619-554-2937

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

mvDF: Acid acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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42.9%; Pred. No. 36;
iive 4; Mismatches
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Gaps

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/note= "The cysteine residues may
be substituted with aminobutyic acid, homocysteine or
dlaminosuberic acid."
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Patent No. 5445932
GENERAL INFORMATION:
APPLICANT: FIELDS, Howard A.
APPLICANT: KHUDYAKOV, Yuri
APPLICANT: KHUDYAKOV, Wichael
TITLE OF INVENTION: METHOD FOR DETECTION OF A NEW MARKER
TITLE OF INVENTION: ASSOCIATED WITH HEPATITIS DELTA VIRUS INFECTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.9%; Score 32; DB 1; Length 24; 42.9%; Pred. No. 72; tive 2; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE PATENTIN STILL SOFTWARE SOFTWARE PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/976,358
FILING DATE: 19921117
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A. PROMATION:
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/134 NIHD
TELECOMMUNICATION INFORMATION:
TELEFRANE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32.5; DE Pred. No. 39; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.2%;
53.8%;
                                                                                                                                                                                                                                                                                                         Modified-site
INFORMATION FOR SEÓ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity 53.6
Matches 7; Conservative
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6 CIKTY-SKPFHPH 17
                                                                                                                                                                                                                                                                                                                                  LOCATION: 4..6
COTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-311-307B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMINO ACID
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
TOPOLOGY:
US-07-976-358-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-976-358-23
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US-08-311-307B-9
US-08-311-307B-9
Sequence 9, Application US/08311307B
Sequence 5.5627156
GENERAL INFORMATION:
TITLE OF INVENTION: Polypeptide Agonist Derived From Human
TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;;
                                                                                                                                                    METHODS FOR PRODUCING POLYPEPTIDE METAL BINDING SITES AND COMPOSITIONS THEREOF
                                                                                                                                                                                                    MUMBER OF SEQUENCES: 65 COMPUTER READABLE FORM: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: ENDORAGIA: 6 COMPUTER: ENDORAGIA: 6 COMPUTER: ENDORAGIA: 6 COMPUTER: PATENTIN FOR COMPUTER: PATENTIN RELATION PATA: 6 COMPUTER: PATENTIN RELATION PATA: 6 COMPUTER: PATENTIN RELATION PATA: 70 FLING DATE: 10 FRE: 1994 PRIOR APPLICATION DATA: 70 FLING DATE: 10 FRE: 10 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 16;
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MEDIUM TYPE: FLOPPY disk
COMPUTER: 1BM PPC COMPATIBLE
COMPUTER: 1BM PC COMPATIBLE
COMPUTER: 1BM PC COMPATIBLE
COMPUTER: 1BM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,307B
FILING DATE: 23-SEP-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
REFERENCE/POCKET NUMBER: 63085
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32.5; DE
Pred. No. 36;
4; Mismatches
                                               Sequence 14. Application PC/TUS9401238 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 amino acids
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Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FRAGMENT TYPE: internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
GY: linear
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Search completed: August 26, 2002, 10:19:36 Job time: 392 sec



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Copyright (c) 1993 - 2000 Compugen Ltd.
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747574 seqs, 111073796 residues 140 1 CGETYQSRVTHPHLPRALMRSTTKC 25 BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-701-623C-5 Perfect score: Scoring table: Sequence: Searched:

253524 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 08 Maximum Match 1008 Minimum DB seq length: 0 Maximum DB seq length: 25

Listing first 45 summaries

/SIDS1/gcgdata/hold-geneser/geneseqp-emb1/AA1991.DAT:* /SIDS1/gcgdata/hold-geneser/geneseqp-emb1/AA1992.DAT:* /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqg-embl/AA1989.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqg-embl/AA1989.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqg-embl/AA198999.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqg-embl/AA1989999.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqg-embl/AA1989999.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqg-embl/AA1989999.DAT:*/SIDSI/gcgdata/hold-geneseq/geneseqg-embl/AA1989999.DAT:*/SIDSI/gcgdata/hold-geneseq/genese /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT: A_Geneseq_032802:* Database :

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:* /SIDS1/gcgdata/hold-genesect/geneseqp-emb1/AA1997.DAT:*/SIDS1/gcgdata/hold-genesect/geneseqp-emb1/AA1998.DAT:*/SIDS1/gcgdata/hold-genesect/geneseqp-emb1/AA1999.DAT:*/SIDS1/gcgdata/hold-genesect/geneseqp-emb1/AA2000.DAT:*/SIDS1/gcgdata/hold-genesect/geneseqp-emb1/AA2001.DAT:*/SIDS1/gcgdata/hold-genesec./geneseqp-emb1/AA2001.DAT:* /SIDS1/gcgdata/hold-geneseq/genesegp-embl/AA1996.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Optimised IqE-CH3	Modified human IqE	Peptide sequence o	Optimised IqE-CH3	Optimised IqE-CH3	Optimised IqE-CH3	IqE peptide antago	IdE peptide antago	Antibody 15A.2 hum	Antibody 15A.2 gre	Human IgE C epsilo
SUMMARIES	AAY79998	AAY91212	AAY68602	AAY79999	AAY80000	AAY80077	AAY42585	AAY42586	AAY50895	AAY50896	AAB26503
DB	21	21	21	21	21	21	20	20	21	21	21
% Query Match Length DB ID	25	25	25	25	25	25	22	24	17	17	19
	100.0	100.0	100.0	77.1	73.6	67.1	66.4	66.4	60.0	57.1	48.6
Score	140	140	140	108	103	94	93	93	84	80	9
Result No.	7	7	m	4	S	9	7	80	6	10	11

Peptide P7X derive IgE peptide #11. Human IgE C epsilo	Peptide P13b deriv Canine immunoglobi	Optimised IgE-CH3	ed ta	15A.		Human IgE C epsilo		Human IgE C epsilo	13	Э	Peptide P13 derive	IgE peptide #16.	Antibody 15A.2 fel	Antibody 15A.2 swi	Human apoptosis re	Human protein frag	#6058	Protein #5684 enco	Human brain expres	Human bone marrow	#	Peptide #6039 enco	Peptide corresp. t	Monoclonal antibod	Antibody 15A.2 bin	Immunogenic peptid		HUPF-I n	Monoclonal antibod	Antibody 15A.2 bin
AAU16830 AAB51033 AAB26518	AAU16849 AAW24102	AAY80001	AAY80048	AAY50893	AAY50894	AAB26517	AAU16848	AAB26519	AAU16850	AAB26516	AAU16847	AAB51038	AAY50897	AAY50898	AAB24095	AAM00660	ABB38552	ABB23685	AAM59175	AAM71710	AAM19280	AAM32002	AAR27321	AAY69599	AAY50891	AAY69579	ABG20283	AAY21389	AAY69600	AAY50892
22 22 21	25 18	21	21	21	21	21	22	21	22	21	22	22	21	21	21	22	22	22	22	22	22	22	13	21	21	21	22	19	21	21
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48. 48. 47.	6 4 4 4	4 45.	4 45.	0 42.	60 42.	41.	8.5 41.		m	37.1	2 3	7		8 34.	2	0 28.	9 27.	9 27.	6	9 27.	9 27.	9 27.	6	7 26.	7 26	7 26	7 26	26	6 25	9
12 13 14	15 16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAY79998 standard; Peptide; 25 AA. 15-MAY-2000) (first entry) AAY79998 AAY79998

Optimised IgE-CH3 domain antigen peptide for human IgE.

Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylaxis; dermathtis.

98US-0100287. 99WO-US13959. Homo sapiens. Synthetic. 21-JUN-1999; WO9967293-A1 20-JUN-1998; 29-DEC-1999.

(UNBI-) UNITED BIOMEDICAL INC. Wang CY, Walfield AM;

WPI; 2000-160578/14.

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy $\mbox{\ \ -}$

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AAY68602
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Exervised
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                                                                                                                                                antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and soo preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucletc acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. (conjugates of (I) that include a promiscuous Thelper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AA779994 to AAX8004 represent amino caid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                      present invention describes immunoglobulin E (IgE)-CH3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 140; DB 21; Best Local Similarity 100.0%; Pred. No. 7.4e-15; Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified human IgE CH3 domain, SEQ ID NO:92.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY91212 standard; peptide; 25 AA.
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                                       Claim 1; Page 21; 155pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNBI-) UNITED BIOMEDICAL INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 AA;
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Intections (HIV, Toot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of lutefinishing hormone releasing hormone (LHRH) for contraception, treatment of hormone—teacher and cancer, prevention of poar taint in meat, and the promise of the promotent cancer; prevention of poar taint in meat, and the promise of immunocastration); for promoting the growth of animals; or for immunocastration); for promoting the gubjects) into an immunogen of immunocastration of a promise of animal of the parameter of improves capacity to induce a strong T helper cell—mediated immune certificates, resulting in production of anithodies against a target aniquent of anithodies against a target aniquent of anithodies and pathogen-derived the head on the measules virus (HBV) protein and sequences ANY91121 represents a promiscuous T helper epitope from hepatitis B virus (HBV) brotein and sequences ANY91121 represents a promiscuous T helper certom hepatitis B virus (HBV) brotein and sequences ANY91125 regulated on the crown hepatitis B virus (HBV) surface antique. ANY91126 regulated and ANY9124 represents a promiscuous The pitope comprising an LHHH sequence joined to a promiscuous The pitope. ANY91197 registed anique sequence joined to a promiscuous The pitope. ANY91197 registed aniques in these LHHH target aniquent peptide used in these LHHH any petitope. ANY91201 somatostatin, and ANY91201-Y91207 are antiqenic peptides. ANY91201 somatostatin, and ANY91201-Y91207 are antiqenic peptides. ANY91201 somatostatin, and ANY91201-Y91207 are antiqenic peptides which may be used to prevent HIV infection of T cells. ANY90121 is a modified version of a human IgE (immunoglobulin E) CH3 domain, and ANY91220 are Th epitope. ANY91221 represent cantigenic peptides which may be used in the treatment of allerytes. ANY91221 and peptides and ANY91222-Y9124 are antigened or the ceptope and may be used in a malarial avaccine ANY9128 Fy91231 represent ceptope and may be used in a malarial avaccine ANY91212 and ANY91221 and are 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesteryl ester transport protein (CETP) or HIV epitopes, but more generally against any pathogen, immunogens may be used for prevention and/or treatment of peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. 7.4e-15;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide sequence of the invention.
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Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes peptide immuncgens comprising a synthetic helper T cell (Th) epitope and a target antigen, luteinising hormone-releasing hormone (LHRH). The peptide immunogens cause hormone-releasing hormone (LHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, oestrus, sexual development and secretion of sex hormones. Provision of a promiscous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide thus high antibody titres against the target antigen. The peptide for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast, also endometriosis); to prevent tumours (cancer of prostate or breast, also endometriosis); to prevent present sequence appears in the specification.
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                                  lutelnising hormone-releasing hormone; spurmatogenesis; ovulation; osstrus; sexual development; sex hormone; promiscuous T helper epitope; vaccine; contraceptive; hormone-dependent tumour; prostate cancer; breast cancer; endometriosis; boar taint; meat quality; immunocastration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammalian LHRH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin B; IqB; epsilon heavy chain: antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthmatic; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide immunogen containing luteinising hormone-releasing hormone antigen site and helper {\tt T} cell epitope, for e.g. contraception and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 140; DB 21;
Pred. No. 7.4e-15;
Mismatches 0;
                Helper T cell epitope; peptide immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 92; 102pp; English.
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Best Local Similarity 100.0%; P
Matches 25; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                  (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                         98US-0100414.
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                                                                                                                                                                                                                                                                                                                         20-JUN-1998;
                                                                                                                                             Unidentified
                                                                                                                                                                                       W09966952-A1
                                                                                                                                                                                                                                (29-DEC-1999.
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Synthetic.
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The present invention describes immunoglobulin E (IgE)-CH3 domain antiperaic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce affer (non-anaphylactogenic) antibodies. RAY79994 to AAY80084 represent anino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                             New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 108; DB 21;
Pred. No. 7.1e-10;
3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 99; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         for immunization against allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY80000 standard; Peptide; 25
                                                                                                                                                                                                                  (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.1%;
72.0%;
                                                                                                       99WO-US13959.
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                                                                                                                                                                                                                                                                     Wang CY, Walfield AM;
                                                                                                                                                                                                                                                                                                                          WPI; 2000-160578/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 AA;
W09967293-A1.
                                               29-DEC-1999
                                                                                                                                                             20-JUN-1998;
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Synthetic.
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The present invention describes immunoglobulin E (1gE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies and anti-asthmatic properties. (I) induces polyclonal antibodies and so preventing triggering and activation of mast cells and basophils and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (incitonal in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disufide bridge) to stabilise conformational features and mainze cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. NAY79994 to NAY80084 represent amino acid sequences used in the exemplification of the present invention.
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                                                  New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy ^{\rm -}
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receptor-binding; binding determinant sequence; anti-IgE antibody;
                                                                                                           Claim 1; Page 146; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGETYQSRVTHPHLPRALMRSTTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY42585 standard; peptide; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.1%;
llarity 64.0%;
Conservative 4
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94US-0178583
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               WPI; 2000-160578/14.
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es 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergic disease.
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07-JAN-1994;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies of antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and so preventing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. (In that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell carget epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AA779994 to AA800084 represent amino cit asequences used in the exemplification of the present invention.
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                                                                                                                                                                New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                          The present invention describes immunoglobulin E (IgE)-CH3 domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.6%; Score 103; DB 21; Length 25; 68.0%; Pred. No. 4.3e-09; Live 3; Mismatches 5; Indels
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                                                                                                                                                                                   for immunization against allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY80077 standard; Peptide; 25
                                                     (UNBI-) UNITED BIOMEDICAL INC.
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                   98US-0100287.
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Best Local Similarity 68.0
Matches 17; Conservative
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                                                                                        Walfield AM;
                                                                                                                             WPI; 2000-160578/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 AA;
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                 20-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                      Wang CY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY80077
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Gaps

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Length 25;

Score 94; DB 21; Length 22.
Pred. No. 1.1e-07;
Sred. Throwes 5; Indels

4; Mismatches

25

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Matches
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                              The invention provides immunoglobulin E (IgE) antagonists comprising one or more of the FcepsilonRI receptor-binding determinant sites of human template antagonists include IgE variants comprising an immunoglobulin template and binding determinant sequences (bds) CDbds, EFbds and the sequence shown in AAY42581. The CDbds (CD loop binding determinant sequence) are selected from the sequences shown in AAY42567. The CDbds (EF loop binding determinant sequences shown in AAY42578 - 442580. The variants are useful in raising and screening anti-IgE antibodies, in the isolation and purification of PcepsilonRI receptor and in the treatment and prophylaxis of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides immunoglobulin E (IJE) antagonists comprising one or more of the FcepsilonRI receptor-bindiny determinant sites of human IGE. The antagonists include IGE variants comprising an immunoglobulin template and bindiny determinant sequences (bds) CDbds, EFbds and the sequence shown in AAY42581. The CDbds (CD ..oop binding determinant sequence) are selected from the sequences shown in AAY4257 and the BFbds (EF loop binding determinant sequences shown in AAY42577 42577 and sequences shown in AAY42578-Y42580. The vai:ants are useful in raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin E variants as peptide antagonists useful for raising and screening anti-immunoglobulin E (19E) anticodies, in the isolation and purification of FcepsilonRI receptor and in the treatment of allergic
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin E; IgE; antagonist; FcepsilonRI receptor; human; bds;
receptor binding; binding determinant sequence; anti-IgE antibody;
allergic disease.
                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                               Length 22;
                                                                                                                                                                                                  Score 93; D3 20; Length 22.
Pred. No. 1.3e-07;
17 Indels
                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 9; 37pp; English.
           Disclosure; Column 9; 37pp; English.
                                                                                                                                                                                                                                                                                                                                              AAY42586 standard; peptide; 24 AA.
                                                                                                                                                                                                               66.48;
94.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-0744768.
                                                                                                                                                                                                                                                             2 GETYQSRVTHPHLPRALM 19
                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                           Local Similarity 94.4 nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                     IgE peptide antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-579941/49.
                                                                                                                                                                              22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-1991;
07-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5965709-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-0CT-1999
                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                       AAY42586;
                                                                                                                                                        diseases
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound igB, and which doesn't bind to IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound igE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.

AMY50876-Y50900 represent peptide mimotopes used in the method of the
and screening anti-IgE antibodies, in the isolation and purification of FcepsilonRI receptor and in the treatment and prophylaxis of allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Binding proteins used for treatment or prophylaxis of canine allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 2.5e-06;
0; Mismatches 1; Indels
                                                                                                                                                      Length 24;
                                                                                                                                                                                               Indels
                                                                                                                                                   Score 93; DB 20; L
Pred. No. 1.5e-07;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody 15A.2 human IgE binding epitope 1.
                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 7; 30pp; English.
                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                               AAY50895 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.0%;
94.1%;
                                                                                                                                                      66.4%;
94.4%;
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99US-0281760
                                                                                                                                                                                                                                                                7 getygcrvthphlpralm 24
                                                                                                                                                                                                                                           2 GETYQSRVTHPHLPRALM 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 QSRVTHPHLPRALMRST 22
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IDEX-) IDEXX LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mermer B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-040833/04
                                                                                                                                            Query Match
Best Local Similarity
Matches 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 AA;
                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP957111-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY50895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                              diseases
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21-DEC-1999;
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       31-AUG-2000
                                                                                        07-AUG-1999
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                                                                                                        29-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-2001
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU16830;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                     This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy.

ANY50876-Y50900 represent peptide mimotopes used in the method of the
                                                                                      Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
epitope; prophylaxis; treatment; mimotope.
                                                                                                                                                                                                                                                                     for treatment or prophylaxis of canine allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    histamine release inhibitor; vaccine; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 80; DB 21; Length 17;
Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                    Antibody 15A.2 green monkey IgE binding epitope 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IgE C epsilon3/4 domain epitope P7.
                                                                                                                                                                                                                                  Mermer B, Francoeur G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä.
                AAY50896 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                      Disclosure; Fig 7; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB26503 standard; Peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IgE; C epsilon3; C epsilon4;
antibody; epitope; mimotope;
                                                                                                                                                                                                                                                                                                                                                                                                                                57.1%;
88.2%;
                                                                                                                                                                                      98US-0058331
99US-0281760
                                                                                                                                                                     99EP-0107035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 QSRVTHPHLPRALMRST 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                LAB INC.
                                                                                                                                                                                                                                                                     Binding proteins used
                                                                                                                                                                                                                                                   WPI; 2000-040833/04
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      17 AA;
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                                                                                                                                                                                                                (IDEX-) IDEXX
                                                   24-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                     09-APR-1999;
                                                                                                                                                                                       09-APR-1998;
                                                                                                                                                                                                30-MAR-1999;
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                                                                                                                                  EP957111-A2
                                                                                                                                                   17-NOV-1999
                                                                                                                                                                                                                                  Lawton R,
                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                      Invention.
                                  AAY50896;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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10
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surface exposed epitope of C epilon3 or C epsilon4 domain of IgE. The epitopes were identified by calculating the accessible surface of each IgE residue. Minotopes were designed to be similar to the epitopes. The epitopes are useful in preparing medicaments for treating or preventing allergies. The epitopes and minotopes of the invention induce anti-IgE antibodies which are capable of raising non-anaphylactic antibodies and inhibiting histamine release. The present sequence is an IgE C epsilon3/4 domain epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides comprising surface exposed epitopes or mimotopes derived from C-epsilon-3 or C-epsilon-4.domains of IgE, useful for preventing or treating allergy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates epitopes and mimotopes of an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; linkage technology; conjugated compound; carrier vehicle; epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E; IgE mediated disease; antibody response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide P7X derived from Cepsilon3/4 region of human IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                        Van Mechelen MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.6%; Score 68; DB 21; I
100.0%; Pred. No. 0.00087;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (PEPT-) PEPTIDE THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU16830 standard; Peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                        Turnell WG,
                                                                       99GB-0017144.
99GB-0018598.
99GB-0018599.
2000WO-EP01456
                                                    99GB-0004408
                                                                                                                                                                                   99GB-0018604
99GB-0018606
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                                                                                                                                                          99GB-0018601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Page 4; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Friede M, Mason S,
Vinals De Bassols YC;
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                                              25-FEB-1999;
21-JUL-1999;
07-AUG-1999;
07-AUG-1999;
07-AUG-1999;
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22-FEB-2000;
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19 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1999;
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07-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                         AAB26518;
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                 14
                                                                                                                                                                                                                                                                                          AAB26518
     οy
                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                               The present invention relates to linkage nethodology for use in the conjugation of compounds (e.g. peptides) to carrier vehicles

(e.g. macromolecules, polymers, dendrimers, proteins) to produce biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition or a vaccine. The protein for use in a pharmaceutical composition or a vaccine. The cinvention describes peptides derived from or mimotopes of the cepsilon3 or cepsilon4 regions of human immunoglobulin E (IgE) which are used to produce conjugated compounds. The compounds or compositions of the invention are useful in the manufacture of a medicament for the treatment of IgE mediated diseases. The invention allows for controlled conjugation of a peritide epitope (antigen) to a protective antibody response in ar animal or human patient. AAU16632-AAU16913 represent peptides derived from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human 1gE.
                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                 A linkage comprising an immunogenic conjugate useful treatment of IgE mediated diseases .
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0
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100.0%; Pred. No. 0.00087;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine; immunoglobulin E; IgE; anti-allergy.
                                           (ACAM-) ACAMBIS RES LTD.
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                  Example 5; Page 25; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB51033 standard; Peptide; 19 AA.
  22-FEB-2000; 2000GB-0004096
22-AUG-2000; 2000GB-0020707,
22-AUG-2000; 2000GB-0020708.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 48.6
Best Local Similarity 100.
Matches 13; Conservative
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                                                                           Flinn N, Johnson T;
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                                                                                               WPI; 2001-521967/57
                                                                                                                                                                                                                                                                                                                                                      19 AA;
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22-FEB-2000;
22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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The present invention relates to a composition comprising allergy peptides inked by an inert carrier. The allergy peptides are derived from Immunoglobulin E (19E) or IgE receptor. The present peptide is one such peptide from IgE. The composition is useful as a vaccine or for manufacturing a medicament for the prophylaxis or treatment of allergy. In particular, for boosting an anti-allergy immune response in an individual susceptible to an allergic response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides comprising surface exposed epitopes or mimotopes derived from C-epsilon-3 or C-epsilon-4 domains of IgE, useful for preventing or treating allergy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
New vaccine comprising allergy peptides linked by an inert carrier, useful for boosting an anti-allergy immune response in an individual susceptible to an allergic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        histamine release inhibitor; vaccine; human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 0.00087;
); Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human IgE C epsilon3/4 domain mimotope P13b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (PEPT-) PEPTIDE THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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100.0%; Pre
0;
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                                                                                                       Claim 5; Page 21; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IgE; C epsilon3; C epsilon4;
antibody; epitope; mlmotope;
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99GB-0017144.
99GB-0018598.
99GB-0018601.
99GB-0018604.
99GB-0018604.
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Best Local Similarity 100.
Matches 13; Conservative
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Vinals De Bassols YC;
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                            The present invention relates epitopes and mimotopes of an isolated surface exposed epitope of C epsilon3 or C epsilon4 domain of IgE. The epitopes were identified by calculating the accessible surface of each IgE residue. Mimotopes were designed to be similar to the epitopes. The epitopes are useful in preparing medicaments for treating or preventing allergies. The epitopes and mimotopes of the invention induce anti-IgE antibodies which are capable of raising non-anaphylactic antibodies and inhibiting histamine release. The present sequence is an IgE C epsilon3/4 domain mimotope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to linkage methodology for use in the conjugation of compounds (e.g. peptides) to carrier vehicles (e.g. macromolecules, polymers, dendrimers, proteins) to produce biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition or a vaccine. The invention describes peptides derived from or mimotopes of the cepsilons, Cepsilons or Cepsilons regions of human immunoglobulin E (IGE) which are used to produce conjugated compounds. The compounds or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an immunogenic conjugate useful treatment of IgE
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide P13b derived as mimotope of Cepsilon3/4 region of human IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; linkage technology; conjugated compound; carrier vehicle; epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E; IgE mediated disease; antibody response.
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                                                                                                                                                                                                                                       DB 21; Length 13; 0.0012; hes 0; Indels
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100.0%; Pred. No.
:ive 0; Mismatch
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(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                              AAU16849 standard; Peptide; 13 AA.
Disclosure; Page 8; 76pp; English
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2000GB-0004096.
2000GB-0020707.
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                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                  1 thphipralmrs 12
                                                                                                                                                                                                                                                                                                    10 THPHLPRALMRS 21
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Best Local Similarity
Matches 12; Conserv
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Synthetic.
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22-AUG-2000;
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compositions of the invention are useful in the manufacture of a medicoment for the treatment of IgE mediated diseases. The invention allows for controlled conjugation of a peptide epitope (antigan) to protein so as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient. AAU16632-AAU1613 represent peptides derived from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.
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100.0%; Pred. No. 0.0012;
ive 0; Mismatches 0; Indels
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Matches 12; Conservative
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August 26, 2002, 10:14:54; Search time 43.94 Seconds '(without alignments) 54.671 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-701-623C-5 140 1 CGETYQSRVTHPHLPRALMRSTTKC 25	BLOSUM62
Title: Perfect score: Sequence:	Scoring table:

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	34	
capex	96089334	
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Total number of hits satisfying chosen parameters:

4981

Minimum DB seq length: 0 Maximum DB seq length: 25

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1p		high conductance c	seed protein ws-6				017	probable acr-2 red	glutathione transf	alpha-1-antichymot	somatotropin - Atl	gene GLUT4 protein	alphaA-conotoxin P	bradykinin-potenti	nerve growth facto	aspartylqlycosamin	monophenol monooxy	bradykinin-potenti	Ig gamma-2b chain	20K protein - rape	genome polyprotein	acetyl-CoA synthet	hypothetical prote	HMG1/2 homolog - a	p7 protein - human	- 5	T-cell receptor al	receptor	T-cell receptor al	conotoxin
SUI		B53145	F61491	A61093	B44379	S29749	PA0054	S72535	S32551	562374	A60621	167422	A58647	н37196	A56901	I37144	A60423	B37196	C30503	S28425	B61409	T44453	T01691	A60975	S41390	A60412	503456	PH0938	S23372	NTKNIM
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seed storage prote NAD(P)H-flavin oxi proteinase inhibit	hypothetical prote intracrystalline c actin-binding prot	tyrosine kinase su brevinin-1 - Frog gaegurin 6 - Korea	cysteine proteinas serine proteinase listeriolysin O -	corticostatic pept glandular kallikre	hypothetical prote hypothetical prote
PA0009 S46241 JA0142	S58382 A56894 PD0015	A56357 JC1355 PC2305	E45087 A60704 B61079	JH0460 A54326	B41868 S30384
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15 18 20	20 20 21	5 5 3	24 25 23	13	15 16
16.4 16.4 16.4	16.4 16.4 16.4	16.4 16.4 16.4	16.4 16.4 16.1	15.7	15.7 15.7
23 23	23 23	23 23 23	23 23 22.5	22	22
30 31 32	33 34 35	36 37 38	39 41 41	42 43	44 45

ALIGNMENTS

RESULT B53145

high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragme C;Species: Bos prinnigenius taurus (cattle) C;Decies: 06-0ct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Jul-2001 C;Accession: B53145	R;Knaus, H.G.; García-Calvo, M.; Kaczorowski, G.J.; García, M.L. ~ ninl. Chem. 269, 3921-3924, 1994 ~ ninl. Chem. 269, 3921-3924, 1994 4140798	SE backbone (NCBIP:144547)
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CBI backbone (NCBIP:144547) activated potassium channel slo

Gaps ; 0 Score 33; DB 2; Length 19; Pred. No. 1.3e+02; 1; Mismatches 4; Indels

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EFYQGSVLNPH 16 9

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RESULT

F61491 seed protein ws-6 - winged bean (fragment) Schoolse: Psophocarpus tetragonolobus (winged bean) C;Date: 07-0ct-1994 #sequence_revision 07-0ct-1994 #text_change 03-May-1996 C;Accession: F61491 R;Hirano, H
J. FIOLETII CIEIII. 8, 113-130, 1989
a mitter of the contract of th

bean seed proteins electroblotted from two-A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-23 <HIR>
C;Superfamily: pathogenesis-related protein
C;Keywords: seed A;Title: Microsequence analysis of winged A;Reference number: A61491; MUID:89351606 A;Accession: F61491

Gaps .<u>`</u> Length 23; Score 32; DB 2; Length 23; Pred. No. 2.3e+02; 3; Mismatches 9; Indels 22.9%; 33.3%; Query Match 22.9 Best Local Similarity 33.3 Matches 6; Conservative

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4 TYQSRVTHPHLPRALMRS 21

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probable acr.2 regulatory leader protein - Neurospora crassa
C; Species: Neurospora crassa
C; Date: 19-Mar. 1998 #sequence_revision 17-Apr-1998 #text_change 21-Jul-2000
C; Accession: 372535
R; Akiyama, M.; Nakashima, H.
Biochim: Biophys. Acta 1307, 187-192, 1996
A; Title: Molecular cloning of the acr-2 gene which controls acriflavine sensitivity in A; Reference number: 372535; MuID:96283814
A; Reference number: S72535
A; Accession: 572535
A; Molecule type: DNA
A; Residues: 1-23 <AKI>
A; Residues: 1-23 <AKI>
A; Cross-references: EMBL:D45893; NID:91754593; PIDN:BAA08306.1; PID:91754594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein QF200017 - fungus (Fusarium sporotrichioldes) (fragment)
C;Species: Fusarium sporotrichioldes
C;Dece: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0054
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Bescription: Two dimensional polyacrylamide gel electropheresis of Fusarium sporotr A;Reference number: PA0054
A;Accession: PA0054
A;Molecule type: protein
A;Residues: 1-15 <CHO>
C;Date: 19-War-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999 C;Accession: S29749 F;Dixon, J.W.; Sarkar, B.
7. Biol. Chem. 249, 5872-5877, 1974 A;Title: Isolation, amino acid sequence and copper(II)-binding properties of peptide A;Accession: S29749; MUID:75011422 A;Accession: S29749 A;Status: preliminary A;Accession: S29749 A;Status: preliminary A;Residues: 1-24 <DIX> C;Superfamily: serum albumin; serum albumin repeat homology
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Pred. No. 9.8e+02;
2; Mismatches 3; Indels
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Pred. No. 8.6e+02;
2; Mismatches 1; Indels
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Best Local Similarity 44.4'
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3 GETQQTKV 10
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                                                                                                                                                                                                                                                                                                                                                                                      A Molecule type: protein
A; Residues: 1-20 < WAI>
A; Note: the amino terminal residue was tentatively identified as Ser
A; Note: 12-Ser was also found
C; Comment: This glue protein is a component of the adhesive plague of the byssus, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: hydroxyproline; tandem repeat
F; 4, 14/Modified site: 3-hydroxyproline (Pro) #status experimental
F; 5, 9, 15, 19/Modified site: 4-hydroxyproline (Pro) #status experimental
F; 7, 11/Modified site: 3', 4'-dihydroxyphenylalanine (Tyr) #status experimental
F; 13/Modified site: 3', 4'-dihydroxyphenylalanine (Tyr) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A. Molecule type: protein
A. Residues: 1-24 < RAM>
A. Cross references: CAS:137706-81-1
A. Cross references: CAS:137706-81-1
A. Cross references: CAS:137706-81-1
C. Commental source: venom
A. Note: sequence extracted from NCBI backbone (NCBIP:116001); structure confirmed by of C. Comment: This omega-conotoxin blocks presynaptic calcium channels.
C. Superfamily: omega-conotoxin blocks presynaptic calcium channels.
C. Stepwords: acetylcholine release inhibition; amidated carboxyl end; calcium channel: F:1-15,8-18,14-23/Disulfide bonds: #status predicted
F:24/Modified site: amidated carboxyl end (Thr) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: B44379
R; Ramilo, C.A.; Zafaralla, G.C.; Nadasdi, L.; Hammerland, L.G.; Yoshikami, D.; Gray, Biochamistry 31, 9919-9926, 1992
A; Title: Novel alpha- and omega-conotoxins from Conus striatus venom.
A; Reference number: A44379; MUID:93003172
A; Accession: B44379
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                                                                                                                                                                                                                                                  R;Walte, J.H.
J. Comp. Physiol. B 156, 491-496, 1986
A;Title: Mussel glue from Mytilus californianus Conrad: a comparative study.
A;Reference number: A61093; MUID:86279063
A;Accession: A61093
                                                                                                                                          N; Alternate names: adhesive polyphenolic protein
C; Species: wytilus californianus (California mussel)
C; Date: 31-Dec.1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C; Accession: A61093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Conus striatus (striated cone)
C;Date: 31-Dec.1993 #sequence_revision 31-Dec-1993 #text_change 23-May-1997
C;Accession: B44379
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Pred. No. 2.9e+02;
4; Mismatches 1; Indels
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                                                                                                                      glue protein - California mussel (fragments)
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C;Species: Canis lupus familiaris (dog)
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Best Local Similarity
Matçhes 4; Conserv
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Best Local Similarity
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C;Accession: A58647
R;Hopkins, C.; Grilley, M.; Miller, C.; Shon, K.J.; Cruz, L.J.; Gray, W.R.; Dykert, J.J. Biol. Chem. 270, 22361-22367, 1995
A;Title: A new family of Conus peptides targeted to the nicotinic acetylcholine recep A;Reference number: A58647; MUID:95403432
A;Accession: A58647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: 167422
R; Olson, A.L.; Edgington, N.P.; Moye-Rowley, W.S.; Pessin, J.E.
Endocrinology 136, 1962-1968, 1995
A; Title: Characterization of 5 -heterogeneity of the rat GLUT4/muscle-adipose glucose
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A; Residues: 1-25 <HOP>
R; Ras, K.H.; Hwang, K.J.; Kim, S.M.; Kim, S.K.; Gray, W.R.; Olivera, B.M.; Rivier, J. R; Han, K.H.; Hwang, K.J.; Kim, S.M.; Kim, Data Bank, December 1996
A; Reference number: A6766; PDB:1PIP
A; Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, rest
B; Han, K.H.; Hwang, K.J.; Kim, S.M.; Kim, S.K.; Gray, W.R.; Olivera, B.M.; Rivier, J. B; Hang, K.J.; Hyang, Hyang
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                                                                                                                                                                                                                                                                                                                                                                                                                     gene GLUT4 protein - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 04-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Conus purpurascens (purple cone)
C;Date: 31-Oct_1997 #sequence_revision 07-Nov-1997 #text_change 15-Sep-2000
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                                 Length 25;
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Score 26; DB 2; Le
Pred. No. 2.1e+03;
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Pred. No. 2.5e+03;
2; Mismatches 4;
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A;Accession: 167422
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C; Superfamily: glucose transport protein
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62.5%;
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41.78;
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66.7%;
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Best Local Similarity
Matches 6; Conserv
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12 NRVQHLHL 19
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A; Residues: 1-25 <RES:
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           S32551
glutchione transferase (EC 2.5.1.18) mu (isojform pI 6.4) - mouse (fragment)
C; Specias: Mus musculus (house mouse)
C; Date: 02-Dec-1993 #sequence_revision 01-Dev: 1995 #text_change 05-Jan-1996
C; Accession: S32551; S32550
R; Singhal, S.S.; Saxena, M.; Ahmad, H.; Awas: hi, Y.C.
Biochim. Biophys. Acta 1116, 137-146, 1992
A; Title: Glutathione S-transferases of mouse liver: sex-related differences in the expre
A; Residues: S32548; MUID: 92256466
A; Accession: S32550
A; Molecule type: protein
A; Residues: 1-13 <SINA>
A; Experimental source: female
A; Accession: S32550
A; Molecule type: protein
A; Residues: 1-13 <SINA>
A; Experimental source: male
C; Keywords: transferase
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362374
alpha-1-antichymotrypsin - human (fragment)
c;Species: Homo sapiens (man)
c;Species: Homo sapiens (man)
c;Species: 1996 #sequence_revision 13-Mar-1997 #text_change 31-Mar-1997
c;Accession: 562374
R;Tsuda, M.; Sel, Y.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Tsuda, T.;
Eur. J. Blochem. 235, 821-827, 1996
A;Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin varia
A;Reference number: 562374
A;Accession: 562374
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-14 <TSU>
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C; Species: Salmo salar (Atlantic salmon)
C; Date: SB.Apr-1993 #sequence_revision 28-Apr-1993 #text_change 30-Sep-1993
C; Accession: A60621
R; Skibeli, V.; Andersen, O.; Gautvik, K.M.
G; Accession: A60621
B; Skibeli, V.; Andersen, O.; Gautvik, K.M.
A; Title: Purification and characterization of Atlantic salmon growth hormone and evidence
A; Title: purification and characterization of Atlantic salmon growth hormone and evidence
A; Reference number: A60621; MUID:91146880
A; Molecule type: protein
A; Residues: 1-25 <SKI>A; Note: this protein displayed charge heterogen; ity from variable levels of phosphorylat
C; Superfamily: prolactin
C; Keywords: hormone; phosphoprotein; pituitary
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Pred. No. 1. Le+03;
3; Mismatches; 1; Indels
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50.0%;
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80.0%;
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4 FMSKVTNP 11
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9 RLTHP 13
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17.9%; Score 25; DB 2; Length 22; 50.0%; Pred. No. 2.6e+03; ive 2; Mismatches 2; Indels
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Best Local Similarity 50.0،
است مبدء 4; Conservative
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5 TFSRRVSH 12
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C;Genetics:
A;Gene: AGU
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C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C:Accession: 137144
R:Park, H:; Vettese, M.B.; Fensom, A.H.; Fisher, K.J.; Aronson, N.N.
Biochem, J. 290, 735-741, 1993
A;Title: Characterization of three alleles causing aspartylglycosaminuria: two from a Br
A;Reference number: 137144; MUID:93207523
                                                                                                                                   bradykinin-potentiating peptide 8 - island jararaca C;Species: Bothrops insularis (island jararaca) C;Species: Bothrops insularis (island jararaca) C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994 C;Accession: H37196 C;Co. Vieira, C.A.; Giglio, J.R. J. Protein Chem. 9 221-227, 1990 J.R. J. Protein Chem. 9 221-227, 1990 J.R. A;Title: Primary structure and biological activity of bradykinin potentiating peptides A;Reference number: A37196; MUD:90351557
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C;Species: Bitis arietans (puff adder)
C;Species: Bitis arietans (puff adder)
C;Species: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Jun-2000
C;Accession: A56901
R;Smith, P.J.; Brandt, W.F.; Stickells, B.J.; von Holt, C.
Comp. Bitchen: Physiol. B 103, 975-980, 1992
A;Title: Bitis arietans nerve growth factor is a disulphide-linked homodimer.
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A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molegule type: mRNA
A;Residues: 1-22 <RES>
A;Residues: 1-22 <RES>
A;Cross-references: EMBL:X73071; NID:9312227; PIDN:CAA51529.1; PID:9312228
                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 CCIN>
C;Reywords: pyrcglutamic acid
F;1/Wodified site: pyrrolidone carboxylic acid (Gln) #status experimental
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A;Status: preliminary
A,Molecule type: protein
A;Residues: 1-21 <SMI>
A;Note: sequence extracted from NCBI backbone (NCBIP:122566)
C;Keywords: disulfide bond; homodimer; venom
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  3 CG-SYPNAACHP 13
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Best Local Similarity
Matches 3; Conserv
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| S HPNIP 9
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us-09-701-623c-5.closed.rsp



Georgian 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 26, 2002, 10:19:40 ; Search time 22.95 Seconds (Without alignments) 42.178 Million cell updates/sec Run on:

US-09-701-623C-5

140 1 CGETYQSRVTHPHLPRALMRSTTKC 25 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapuxt 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

1503 Total number of hits satisfying chusen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 25

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 surmaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	tre	conus purp	bothro		0422	_	P21794 rattus norv	P01521 conus maqus	74 pinus	4 tetrak	_	P32423 rana brevip	P80400 rana rugosa	Q05564 klebsiella	Q02210 pseudomonas		P56587 apis mellif		P24335 trimeresuru	P32560 cavia porce	conns	Q92060 gallus gall	P81464 bombus pasc	P82694 periplaneta		P80491 methanosarc	-s	2536	æ		P22702 neurospora	022 polyodon s	P15471 conus stria
SUNMARIES	ID	FP	CXA4_CONPU	BPP8_BOTIN	MI17_BOVIN	BPP2_BOT.IN	MCA2_RHOOP	HI70_RAT	CXA1_CONMA	UN05_PINP:3	FA71_TETPY	SODM_RANCA	BR1_RANBP	GAE6_RANRU	MALE_KLEPN	YMOR_PSEPU	MIF_PIG	TERT_APIME	BR1A_RANES	TX12_TRIWA	NEUT_CAVPO	CXA1_CONCN	MAOX_CHICK	APID_BOMPA	PH1_PERAM	CXA2_CONST	FRHG_METBA	CS21_STRTR	TL18_SPIOL	THAN_PODMA	FEDG_AMYME	Y3KD_NEUCR	മ	CXA1_CONST
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P28467 acinetobact P01519 conus geogr P22799 enterobacte P81106 pinus pinas P56638 conus episc P30800 octopus vul P81527 pasteurella P82616 equus cabal P45440 streptomyce P82976 mus musculu Q9y710 schizosacch P41489 locusta mig
15 1 ACEA_ACICA 15 1 CXA1_CONGE 15 1 SOME ENTRAE 15 1 UNO1 PINPS 16 1 CXA1_CONEP 18 1 AZA_OCTVU 20 1 SODE_PASPI 23 1 ALLS_HORSE 24 1 LERR STRFR 25 1 GBX1_MOUSE 25 1 RL41_SCHPO 9 1 LMT3_LOCMI
20 14.3 20 14.3 20 14.3 20 14.3 20 14.3 20 14.3 20 14.3 20 14.3 20 14.3 20 14.3
33 3 3 3 4 4 4 4 4 4 4 4 4 4 5 5 5 5 5 5

ALIGNMENTS

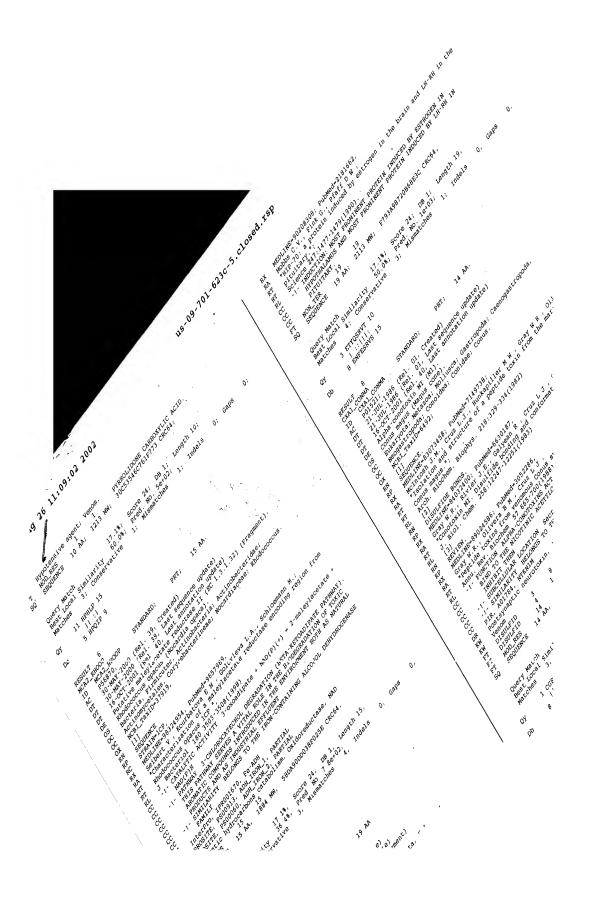
CXA4_CONPU STANDARD; PRT; 25 AA.
P55663;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Alpha-A conotoxin PIVA.
Conus purpurascens (Purple cone).
Eukaryota, Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.

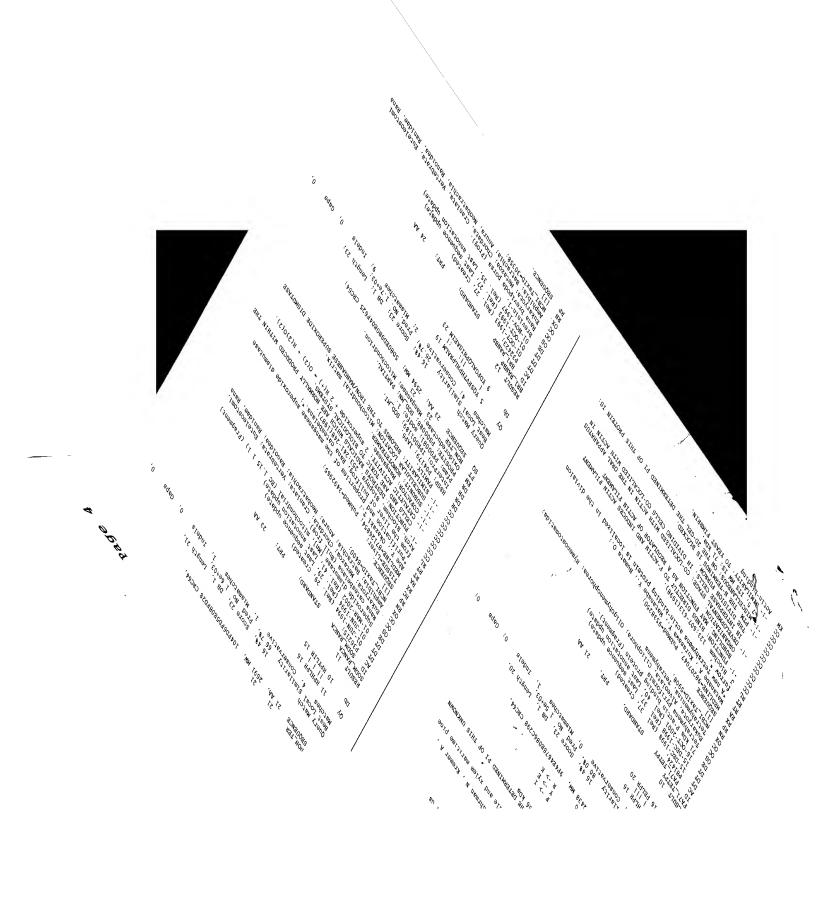
[1] SEQUENCE. TISSUE-Venom; MEDLINE-95403432; PubMed-7673220;

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MEDLING-90311557; PubMed-2386615;
Cintra A.C.O., Vieira C.A., Giglio J.R.;
Cintra A.C.O., Vieira C.A., Giglio J.R.;
Frimary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
J. Protein Chem. 9:221-227(1990).
-!-FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN CONVERTING ENZYME AND ENHANCES THE ACTIVITY OF THE BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
PIR; B37196; B37196.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last sequence update)
Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting enzyme inhibitor).
Buchrops insularis (Island jararaca) (Queimada jararaca).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
17 kDa milk glycoprotein (Fragment).
Bos taurus (Bovine).
Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bos.
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Pred. No. 7.4e+02;
Mismatches 5; Indels
                                    Indels
Pred. No. 3.5e+02;
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                                      2; Mismatches
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MEDLINE-93308294; PubMed-8320368;
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               60.08;
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26.7%;
                                    3; Conservative
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                                                                       11 HPHLP 15
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| HPNIP 9
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ID MI17_BOVIN
AC P35451;
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P30422;
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                                                                                                                                                               Han K.-H., Hwang K.-J., Kim S.-M., Kim S.-K., Gray W.R., Olivera B.M., Rivier J., Shon K.-J.; "NMR structure determination of a novel conotoxin, [Pro 7,13] alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Venom;
MEDLING-90331557; PubMed-2386615;
Cintra A.C.O., Vleira C.A., Giglio J.R.;
Cintra A.C.O., Vleira C.A., Giglio J.R.;
Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
J. Protein Chem. 9:22-227(1990)
J. Protein Chem. 9:21-227(1990)
I. PROCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADKININI BY INDIRECT HYPOTENSIVE AGENT.

IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
PIR: H37196, H37196
                                                                                                                                                                                                                                                                                                                                                              Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation; Hydroxylation; Venom; 3D-structure.
DISGLEID 2 16
DISGLEID 3 11
DISGLEID 14 23
MOD_RES 7 7 HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
               Hopkins C., Grilley M., Miller C., Shon K.-J., Cruz L.J., Gray W.R., Dykert J., Rivier J., Yoshikami D., Olivera B.M.;
"A new family of Conus peptides targeted to the nicotinic acceptor.", as acceptor.", Biol. Chem. 270:22361-22367(1995).
                                                                                                                                                                                                                     A-conotoxin PIVA.";
Biochemistry 36:1669-1677(1997).
-I- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
INHIBIT THEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bothrops insularis (Island jararaca) (Queimada jararaca).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosuuria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crocalinae; Bothrops.
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
enzyme inhibitor).
                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
PDB; 1P1P; 07-JUL-97.
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9E2147898D697640 CRC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                              MEDLINE=97200721; PubMed=9048550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypotensive agent; Venom.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGETYQSRVTHP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CG-SYPNAACHP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 5: Conserv
                                                                                                                               STRUCTURE BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BPP8_BOTIN
P30426;
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SEOUENCE
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SEQUENCE

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                                                           Bachellier S., Perrin D., Hofnung M., Gilson E.; "Backerial interspersed mosaic elements (BIMEs) are present in the genome of Klebsiella "; Mol. Microbiol. 7:537-544(1993).

-!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE TRANSPORT SYSTEM: INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND CHEMOTAXIS TOWARD MALTOOLIGOSACCHARIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Periplasmic.
SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
PROTEIN FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93199531; PubMed-8452544;
MPDLINE-93199531; Caswell D.A., Lowe C.R., Bruce N.C.;
"Nucleotide sequence and over-expression of morphine dehydrogenase,
plasmid-encoded gene from Pseudomonas putida M10.";
Biochem. J. 290:539-544(1993).
                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Maltose-binding periplasmic protein (Maltodextrin-binding protein)
                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8FD8DC4415A6DDDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in MORA 3'region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000567; SBP_bac_1.
PROSITE; PS01037; SBP_BACTERIAL_1; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transport; Sugar transport; Periplasmic.
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                                                                                                                                                                                                                                                    STRAIN=1033-5P14 / KAY2026;
MEDLINE=93211295; PubMed=8459773;
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(Rel. 29, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.7%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                      Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas putida.
Plasmid pMDH7.2.
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                   (MMBP) (Fragment)
                                                                                                                                                                                             NCBI_TaxID=573;
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5 QSRIT
                                                                                                                                                                               Klebsiella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-M10;
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YMOR_PSEPU
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                                                                                                                                                      HIGH HEMOLYTIC ACTIVITY.
--!- SUBCELLIALMAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: SKIN.
-!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Siochem. Biophys. Res. Commun. 205:948-954(1994).
1- FUNCTION: HAS A NON-HEMOLYTIC ACTIVITY. HAS A BROAD SPECTRUM OF
ACTIVITY AGAINST BOTH GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: SKIN. SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
                                    Morikawa N., Hagiwara K., Nakajima T.;
"Brevinin-1 and -2, unique antimicrobial peptides from the skin of
the frog, Rana brevipoda porsa.";
Biochem. Blophys. Res. Commun. 189:184-190(1992).
-!- FUNCTION: SHOWS ANTIBACTERTAL ACTIVITY AGAINST REPRESENTATIVE
GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIAL SPECIES, AND A VERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rana rugosa (Wrinkled frog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Raniae; Rana.
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Park J.M., Jung J.-E., Lee B.J.;
"Antimicrobial peptides from the skin of a Korean frog, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.4%; Score 23; DB 1; Length 24; 33.3%; Pred. No. 1.8e+03; Live 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB 1; Length 24;
Pred. No. 1.8e+03;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                        Length 24;
                                                                                                                                                                                                                                                                                             18 24 BY SIMILARITY.
24 AA; 2531 MW; C866285B191EFDF4 CRC64;
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09918123FF90CCFD CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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DISULFID 18 24 BY SIMILA
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                      MEDLINE=93080555; PubMed=1449472;
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33.3%;
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24 AA; 2610 MW;
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13 VPALFCKITKKC 24
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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TISSUE=Skin;
TISSUE=Skin;
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P80400;
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MALE_KLEPN
ID MALE_KLEPN
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Gaps

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Length 10; Indels

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09ps29 bitis ariet
013726 homo sapien
09fs20 nitrosomona
095s95 drosophila
099162 moema staec
099162 moema staec
09418 oryza sativ
P82871 rana sylvat
064341 mus musculu
09xsg1 bos taurus
094210 solanum tub
09pus pseudomonas
09qus mus sp. erp
09w9ul simian herp
09v9ul simian herp
09v9ul simian herp
09v655 simian herp
09v6180 pseudomonas
04fs18 lumbricus r
033294 zea mays (m
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096w02 fusarium ox
013659 homo sapien
094781 trypanosoma
                           Q9r1f0 mus musculu
                                           P82232 rana tempor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim S., Kweon O.K., Kim Y., Kim C.K., Lee K.S., Kim Y.C.;
"Localization and sequence analysis of the phnH gene encoding 2-hydroxypent-2,4-dienoate hydratase in Pseudomonas sp. strain DJ77.";
Blochem. Biophys. Res. Commun. 238:56-60(1997).

NON_TER. 1

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NON_TER.
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
2-HYDROXYMUCONIC SEMIALDEHYDE DEHYDROGENASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 AA; 2203 MW; 4E913B3E1212214B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 2;
Pred. No. 3e+02;
1; Mismatches
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MEDLINE-97445124; PubMed-9299451;
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60.0%;
   Sphingomonas chungbukensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 22.1
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
11 HPHLPRALMR 20
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HQHLRKALRR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sphingomonas.
NCBI_TaxID=56193;
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Q9TR98;
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Q9TR98
ID Q9
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034216
g
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P95839 staphylococ
0910c6 gallinula c
090zv4 rallus limi
090zv2 rallus long
090zv2 sarothrura
09ubt0 homo sapien
09bqt0 homo sapien
013665 homo sapien
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052321 escherichia
073337 human immun
042416 gallus gall
09buh0 homo sapien
016310 homo sapien
                                                                                                               (without alignments)
69.509 Million cell updates/sec
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                                                                                                August 26, 2002, 10:18:45; Search time 62.22 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                               562222 segs, 172994929 residues
                                                                                                                                                       US-09-701-623C-5
140
1 CGETYQSRVTHPHLPRALMRSTTKC
                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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013BCT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Rallus.
NCBI_TaxID=156759;
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Rallus longirostris (clapper rall).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria: Aves; Neognathae; Gruiformes; Rallidae; Rallus.
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 Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Gallinula
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Shapiro L.H., Dumbacher J.P.;
"Adenylate kinase intron 5: a new nuclear locus for avian
                                          SEQUENCE FROM N.A.
Shapiro L.H., Dumbacher J.P.;
"Adenylate kinase intron 5: a new nuclear locus for avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27; DB 13; Length 22
Pred. No. 1.7e+03;
4; Mismatches 5; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Pred. No. 1.7e+03;
4; Mismatches 5;
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Auk 118:248-255(2001).
EMBL: AF972551: AAK43728.1; -
EMBL: AF372550; AAK43728.1; JOINED.
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis
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0910C6 (TrEMBLAEL 19, Created)
01-DEC-2001 (TrEMBLAEL 19, Last sequence update)
01-DEC-2001 (TrEMBLAEL 19, Last annotation update)
ADBYLATE KINASE (FRAGMENT)
03-DEC-2001 (TREMBLAEL 19, Last annotation update)
ADBYLATE KINASE (FRAGMENT)
03-DEC-2001 (TREMBLAEL 19, Last annotation update)
ADBYLATE KINASE (FRAGMENT)
03-DEC-2001 (TREMBLAEL 19, Last annotation update)
Callinula chicropus (Common moorhen).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                 "Plasma proteins as early biomarkers of exposure to carcinogenic aromatic amines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu S., de Lencastre H., Tomasz A.;
"Sigma-B, a putative operon encoding alternate sigma factor of
Staphylococcus aureus RNA polymerase: molecular cloning and DNA
                                                                                                                                                       Miller M.J., Parmelee D.C., Benjamin T., Sechi S., Dooley K.L.,
Kadlubar F.F.;
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Pred. No. 9e+02;
2; Mismatches 3; Indels
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Pred. No. 1.2e+03;
0; Mismatches 2; Indels
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SEQUENCE 17 AA; 2024 MW; 1D39F70F7D23B269 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 AA; 2541 MW; 7F47717B1767D34F CRC64;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ALBUMIN (FRAGMENY).
Canls familiaris (Dog).
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Last annotation update)
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Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBL_TaxID=1280;
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EMBL; Y09929; CAA71063.1; -.
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MEDLINE-95007849; PubMed-7923441;
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MEDLINE-96427339; PubMed-8830703;
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Similarity 44.4%;
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
6-PHOSPHOFRUCTO-2-KINASE/FRUCTOSE-2, 6-BISPHOSPHATASE (EC 2.7.1.105)
                                                                                                                                                                                                                                                                                         Sarothrura elegans.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Sarothrura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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"Identification of the Promoter Region of Human Placental 6-
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Shapiro L.H., Dumbacher J.P.;
"Adenylate kinase intron 5: a new nuclear locus for avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 22;
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           "Adenylate kinase intron 5: a new nuclear locus for avian
                                                                                                             Score 27; DB 13; Length 22
Pred. No. 1.7e+03;
4; Mismatches 5; Indels
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Pred. No. 1.7e+03;
4; Mismatches 5; Indels
                           Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307901; AAK43539.1; -.
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22 22
22 AA; 2447 MW; CBOCFBB55B82C2A8 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAY-2000 (TrEMBLrel. 13, Last anno
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Shapiro L.H., Dumbacher J.P.;
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30.8%;
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Auk 118:248-255(2001).
EMBL; AF307902; AAK43540.1;
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MEDLINE-21195339; PubMed-11297743;
MEDLINE-21195339; PubMed-11297743;
MEDLINE-21195339; PubMed-11297743;
MEDLINE-21195339; PubMed-11297743;
Median R., Berger W.;
A small upstream open reading frame causes inhibition of human major vault protein expression from a ubiquitous mRNA splice variant.";
FEBS Lett. 494:99-104(2001).
FEBML, A3291367; CAS3315.1; -.
Hypothetical protein.
SEQUENCE 18 AA; 2179 MW; 5D06F9A3F11CB828 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 2.2 KDA PROTEIN.
HYPOTHETICAL 3.2 KDA PROTEIN.
HOWO Saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                        SEQUENCE FROM N.A.
Mahlknecht U., Bucala R.;
Mahlknecht U., Bucala R.;
Homo sapiens inducible 6-phosphofructo-2-kinase/fructose-2,6-
bisphosphatase (IPFK2), genomic sequence.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR033994; BAA89551.1;
EMBL; AF110958; AAA39991;
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Phosphofructo-2-kinase/Fructose-2,6-bisphosphatase Gene Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 25 AA; 2984 MW; 4ACC24B43FDBB74C CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
CARDIAC MYOSIN BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                            Score 27; DB 4;
Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                             19.3%; Sco...
40.3%; Pred. No. c.
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Pred. No.
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100.0%; Pre
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SEQUENCE FROM N.A.
MEDLINE=96083592; PubMed=7493025;
                                                                                                                                                                                                                                                                                                                                                                                               3 ETYQSRVT-----HPHLPR 16
                                                                                                                                                                                                                                                                                                                                                                                                                         4 ELTQSRVQKIWVPVDHRPSLPR 25
                                                                                                                                                                                                                                                                                                                                                      9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                         Kinase; Transferase
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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les 4; Conserv
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STRAILING 1 C188MC;
MEDLINE=96069819; PubWed=7481804;
Deacon N.J., Tsykin A., Solomon A., Smith K., Ludford-Menting M.,
Hooker D.J., Morbhee D.A., Greenway A.L., Ellett A., Chatfield C.,
Lawson V.A., Crowe S., Maerz A., Sonza S., Learmont J., Sullivan J.S.,
Cunningham A., Dwyer D., Dowton D., Mills J.;
"Genomic structure of an attenuated quasi species of HIV-1 from a
blood transfusion donor and recipients.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     042416
042416;
042416;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
THROMBOMUCIN (FRAGMENT).
Gallus (Ghicken).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97444372; PubMed-9298993;
McNgny K.M., Pettersson I., Rossi F., Flamme I., Shevchenko A.,
Mann M., Graf T.;
"Thrombomucin, a novel cell surface protein that defines thrombocytes
and multipotent hematopoietic progenitors.";
                                                                                                                                                                            Gaps
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                                                                                                                                          Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U37270; AAC54551.1; -.
SEQUENCE 24 AA; 2760 MW; 108D5DB2E4F7B73D CRC64;
                                                                                        17351FBF990C1827 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 26; DB 15; Le
Pred. No. 2.7e+03;
3; Mismatches 6;
                                                                                                                                      18.6%; Score 26; DB 2; I 54.5%; Pred. No. 2.6e+03; ive 1; Mismatches 4;
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   Biochem. Soc. Trans. 16:942-943(1988).
EMBL; M27782; AAA56854.1; -.
Plasmid.
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35.7%;
                                                                                        2436 MW;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 18.6
Best Local Similarity 35.7
Matches 5; Conservative
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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23
23 AA;
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Matches 6; Conser
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Watkins H., Conner D., Thierfelder L., Jarcho J.A., MacRae C., McKenna W.J., Maron B.J., Seldman J.G., Seldman C.E.; Mutations in the cardiac myosin binding protein-C gene on chromosome 11 cause familial hypertrophic cardiomyopathy."; Nat. Genet. 11:434-437(1995).

BMBL; S80805; AAB35661.1; -

SEQUENCE 18 AA; 1891 MW; 3EC842CE85A19C97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicolas M.G., Fujiki K., Murayama K., Suzuki M.T., Mineki R.,
Hayakawa M., Yoshikawa Y., Cho F., Kanai A.,
"Studies on the mechanism of early onset macular degeneration in
cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations
of two proteins in the retina.";
Exp. Eye Res. 62:211-219(1996).
SEROUENCE 20 AA: 2411 MW: 5F1A6AEB5918F777 CRC64;
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALBUMIN (FRAGMENT).

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia,
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MEDLINE-89137712; PubMed-3265670;
Price C., Bickle T.A.;
"Evolution of DNA sequence specificity in type I restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 6; Length 20;
Pred. No. 2.2e+03;
3; Mismatches 2; Indels
                                                                                                                                                                            Length 18;
                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                    O9TO26;
U-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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Last annotation update)
                                                                                                                                                                         Score 26; DB 4;
Pred. No. 2e+03;
); Mismatches
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50.0%;
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                                                                                                                                                        Ouery Match
Best Local Similarity 50.0.
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                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae; Macaca.
NCBI_TaxID=9541;
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Best Local Similarity
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                                                                                                                                                                                                                                                                      9 CGGIYVCRAT 18
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Gaps
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Q9BUH0;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 2.6 KDA PROTEIN.
HYPOTHETICAL 2.6 KDA PROTEIN.
HOMO SAPPLOS (Human).
EUKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
WNBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                              Query Match
18.2%; Score 25.5; DB 13; Length 19;
Best Local Similarity 42.9%; Pred. No. 2.5e+03;
Matches 6; Conservative 2; Mismatches 1; Indels
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Pred. No. 3e+03;
1; Mismatches 5; Indels
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TISSUE-BRIOMETRIAL ADENOCARCINOMA;
Strausberg FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002629; AAH02629.1; -.
Hypothetical protein.
SEQUENCE 22 AA; 2645 MW; 60B9F471AB613874 CRC64;
J. CALL Biol. 138:1395-1407(1997).

EMBL, Y13977; CAA74310.1; -.

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SEQUENCE 19 AA; 2181 MW; 483C3DF97E13EC19 CRC64;
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Best Local Similarity 53.3%;
Matches 8; Conservative
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09BUH0
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Search completed: August 26, 2002, 10:29:34 Job time: 649 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein - protein search, using sw model

August 26, 2002, 10:20:41; Search time 43.94 Seconds (Without alignments) 54.671 Million cell updates/sec Run on:

US-09-701-623C-6

Title: Perfect score:

25 141 1 CGETYYSRVTHPHLPKDIVRSIAKC Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues

Searched:

4981 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 25

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:* Database :

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ø			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
П	29	20.6	20	~	A61093	alue protein - Cal
7	28	19.9	11	7	S78765	omal prote
3	28	19.9	23	7	F61491	seed protein ws-6
4	27	19.1	15	7	C37765	hypothetical prote
S	27	19.1	17	7	PH1802	T cell receptor al
9	27	19.1	19	7	B53145	high conductance c
7	27	19.1	19	7	E49048	T-cell receptor be
œ	27	19.1	20	7	A41439	acid ribonuclease
σ	26.5	18.8	25	7	A58647	alphaA-conotoxin P
10	26	18.4	13	~	S32551	qlutathione transf
11	26	18.4	-	7	PH1628	Iq H chain V-D-J r
12	26	18.4	-	4	I38336	hypothetical TEL/M
13	26	18.4	П	7	PH1634	Iq H chain V-D-J r
14	26	18.4	7	7	A60621	somatotropin - Atl
15	25	17.7	10	7	н37196	
16	25	•	14	7	S62374	alpha-1-antichymot
17	25	17.7	15	7	PA0071	superoxide dismuta
18	25	•	15	7	I50503	agrin - electric r
19	25	17.7	17	7	S69164	ferredoxin al - Ja
20	25		21	7	B33600	glutamateammonia
21	25		22	7	PH1359	Iq heavy chain DJ
22	25	17.7	22	~	T01859	CYI la protein - c
23	25	17.7	23	~	S72535	probable acr-2 reg
24	25		24	~	B44379	omega-conotoxin SV
25	25	17.7	24	N	S29749	serum albumin - do
56	25	17.7	24	~	G85602	hypothetical prote
27	25	17.7	25	~	PH1686	Ig heavy chain V r
28	24.5	17.4	23	~	S23637	hypothetical prote
29	24	17.0	10	7	B37196	bradykinin-potenti

T-cell antigen recubioning	mitogen requiated	outer layer protei	cytochrome-b5 redu	alpha-amylase inhi	nicotinic acetylch	T-cell receptor al	alpha-conotoxin Cn	Ig heavy chain CRD.	alpha-conotoxin MI	seed storage prote	hypothetical prote	superoxide dismuta	proteinase inhibit	monocyte chemotact
S47358 S42741	149425	S23981	S42567	S48156	A25738	503456	A58963	PT0301	NTKN1M	PA0009	C85956	PA0012	JA0142	167551
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17.0 13	17.0 17	17.0 20	17.0 22	17.0 23	17.0 24	17.0 25	16.7 14	16.3 11	16.3 14	16.3 15	16.3 17	16.3 19	16.3 20	16.3 20
24 17.0 13	24 17.0 17	24 17.0 20	24 17.0 22	24 17.0 23	24 17.0 24	24 17.0 25	23.5 16.7 14	~	23 16.3 14	23 16.3 15	23 16.3 17	23 16.3 19	23 16.3 20	23 16.3 20

ALIGNMENTS

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Willernate names: adhesive polyphenolic protein
C;Species: Mytilus californianus (California mussel)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C;Accession: A61093
R;Waite, J. H.
J. Comp. Physiol. B 156, 491-496, 1986
A;Title: Mussel glue from Mytilus californianus Conrad: a comparative study.
A;Reference number: A61093; MUD:86279063
A;Molecule type: protein
A;Residues: 1-20 <WAI>
A;Molecule type: protein
A;Note: the amino terminal residue was tentatively identified as Ser
A;Note: 12-Ser was also found
C;Comment: This glue protein is a component of the adhesive plaque of the byssus, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: hydroxyproline; tandem repeat
F;4,14/Modified site: 3-hydroxyproline (PrO) #status experimental
F;5,9,15,19/Modified site: 4-hydroxyproline (PrO) #status experimental
F;7,17/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental
F;13/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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Pred. No. 8.2e+02;
4; Mismatches 3; Indels
glue protein - California mussel (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.6%;
40.0%;
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Best Local Similarity 40.0
Matches 6; Conservative
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4 TYYSRVTHP--HLPK 16

|| ::|:| : || 6 TYKPKITYPPTYKPK 20 qq à

S78765

Schools protein MRP-S24, mitochondrial - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20.5ep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78765
R;Graack, H.R.
Submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Accession: S78765
A;Accession: S78766
A;Accession: S78765
A;Accession: S78766
A;Accession: S78765
A;Accessi

Length 11;

Score 28; DB 2; Pred. No. 6.1e+02; 19.9%; 40.0%; Query Match Best Local Similarity

26 11:09:14 2002

Mon Aug

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high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragme C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Daces (Coct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Jul-2001
C; Accession: B53145
R; Knaus, H.G.; Garcia-Calvo, M.; Kaczorowski, G.J.; Garcia, M.L.
J; Biol. Chem. 269, 391-3924, 1994
A; Title: Subunit composition of the high conductance calcium-activated potassium chan A; Reference number: A53145; MUID:94140798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragmen
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A41439
A216 ribonuclease (EC 3.1.-.-) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 21-Mar-1996
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A;Residues: 1-19 <KNA>
A;Note: sequence extracted from NCBI backbone (NCBIP:144547)
C;Superfamily: fruit fly calcium-activated potassium channel slo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.1%; Score 27; DB 2; Length 19; 66.7%; Pred. No. 1.5e+03;
                                                                                     Length 17;
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45.5%; Pred. No. 1.5e+03;
ive 1; Mismatches 5;
                                                                                  Score 27; DB 2; Le
Pred. No. 1.4e+03;
0; Mismatches 2;
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                                                                                     19.18;
71.48;
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Best Local Similarity 45.5
Matches 5; Conservative
                                                                                     Query Match 19.1
Best Local Similarity 71.4
Matches 5; Conservative
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EFYQGSVLNPH 16
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Best Local Similarity
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A; Status: preliminary
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3 CGERPYS
A; Molecule type:
A; Residues: 1-17
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C;Species: Chloroflexus aurantiacus
C;Species: Chloroflexus aurantiacus
C;Species: Chloroflexus aurantiacus
C;Species: Choroflexus aurantiacus
C;Accession: C37765
R;Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.
Bacteriol. 172, 4497-4504, 1990
A;Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus aurantiacus
A;Reference number: A37765; MUID:90330558
A;Accession: C37765
                                                                                                                                                                                                                                                                                                      J. Protein Chem. 8, 115-130, 1989
Ayîtle: Wicrosequence analysis of winged bean seed proteins electroblotted from two-dim
A;Reference number: A61491; MUID:89351606
A;Accession: F61491
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C;Species: Psophocarpus tetragonolobus (winged bean)
C;bate: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 03-May-1996
C;Accession. F61491
R;Hirano, H.
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Pred. No. 1.3e+03;
3; Mismatches 10; Indels
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Pred. No. 1.2e+03;
0; Mismatches 3; Indels
  Indels
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e
  Mismatches
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A;Molecule type: protein
A;Residues: 1-23 <HIR>
C;Superfamily: pathogenesis-related protein
C;Keywords: seed
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A;Accession: PH1802
A;Status: preliminary
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19.9%;
Best Local Similarity 31.6%;
Matches 6; Conservative
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Best Local Similarity 62.5%;
Matches 5; Conservative
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  4; Conservative
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A;Molecule type: DNA
A;Residues: 1.15 <THE>
A;Cross-references: GB:M33964
                                         11 HPHLPKDIVR 20
                                                                                  2 HVDVPKDLTK 11
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1658
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less m A;Reference number: PH1580; MUID:93301609
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C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C;Accession: 13836
R;Buljs, A.; Shorr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A Oncogene 10, 1511-1519, 1995
A;Tile: Translocation (12,22) (p13:q11) in myeloproliferative disorders results in f A;Reference number: 138031; MUID:95249265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-15 <BUI>
A; Cross-references: EMBL:X85026; NID:g971473; PIDN:CAA59399.1; PID:g971474
C; Comment: This sequence is the chimeric product of a translocation mutation.
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Pred. No. 1.7e+03;
1; Mismatches 1;
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A;Molecule type: DNA
A;Residues: 1-14 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
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A;Status: translated from GB/EMBL/DDBJ
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80.0%;
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Similarity 66.7%;
4; Conservative
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                   A; Experimental source: female A; Accession: $32550
                                                                                          A;Molecule type: protein
A;Residues: 1-13 <SIN2>
A;Experimental source: male
C;Keywords: transferase
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A,Map position: 22q11/12p13
C,Keywords: fusion protein
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Best Local Similarity
Matches 4; Conserv
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6 HLPHDL 11
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9 RLTHP 13
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Matches
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A. Residues: 1-25 (HOP>
A. Residues: 1-25 (HOP>
B. Residues: 1-25 (HOP>
R. Han, K.H.; Hwang, K.J.; Kim, S.M.; Kim, S.K.; Gray, W.R.; Olivera, B.M.; Rivier, J.; S. R. Reference number: A67666; PDB.1PIP
A. Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
R. Han, K.H.; Hwang, K.J.; Kim, S.M.; Kim, S.K.; Gray, W.R.; Olivera, B.M.; Rivier, J.; B. A. Title: NMR structure determination of a novel conotoxin, [Pro 7,13] alpha A-conotoxin
A. Fitle: NMR structure determination of a novel conotoxin, [Pro 7,13] alpha A-conotoxin
A. Fitle: NMR structure determination and disulfide bond assignments by (1)H-NMR
C. Superfamily: unassigned conotoxins
C. Superfamily: unassigned conotoxins
C. Superfamily: unassigned conotoxins
C. Superfamily: anotoxinfide bonds: #status experimental
F. 7,13/Modified site: 4-hydroxyproline (Pro) (Partial) #status experimental
F. 7,13/Modified site: 4-hydroxyproline (Pro) #status experimental
F. 25/Modified site: amidated carboxyl end (Gln) #status experimental
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R;Hopkins, C.; Grilley, M.; Miller, C.; Shon, K.J.; Cruz, L.J.; Gray, W.R.; Dykert, J.;
R;Hopkins, C.; Grilley, M.; Miller, C.; Shon, K.J.; Cruz, L.J.; Gray, W.R.; Dykert, J.;
A;Title: A new family of Conus peptides targeted to the nicotinic acetylcholine receptor A;Reference number: A58647; MUID:95403432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expre
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C;Species: Conus purpurascens (purple cone)
C;Date: 31-Oct_1997 #sequence_revision 07-Nov-1997 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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C;Accession: A41439
R;Ohgi, K.; Sanda, A.; Takizawa, Y.; Irie, M.
J. Biochem. 103, 267-273, 1988
A;Title: Purification of acid ribonucleases from bovine spleen.
A;Reference number: A41439; MUID:88227899
A;Status: preliminary
A;Mesidues: 1-20 <OHG>
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
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Pred. No. 1.6e+03;
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Matches 4; Conservative
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Matches 7; Conservative
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9 HLYFPKDL 16
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17.7%; Score 25; DB 2; Length 10; 60.0%; Pred. No. 1.5e+03; ive 2; Mismatches 0; Indels
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Query Match
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Matches 3; Conservative
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5 HPNIP 9
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                                                                                                                   Ig H chain V-D-J region (clone B-less 213) - mouse (fragment)
(Species: Mus musculus (house mouse)
(Species: Mus musculus (house mouse)
(Spate: O'Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
(Stacession: PH1634
(R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
(B:Levinson, D.A.; Campos-Torres, J.; Leder, P.
(A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice)
(A:Reference number: PH1580; MUID:93301609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NyAlternate names: growth hormone (Species: Salmo salar (Atlantic salmon) (C)Species: Salmo salar (Atlantic salmon) (C)Species: Salmo salar (Atlantic salmon) (C)Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 30-Sep-1993 (C)Accession: A60621 (C)Accession: A60621 (C)Accession: A60621 (C)Accession: A60621 (C)Accession: A60621; MUID: 1990 (C)Accession: A60621 (C)Accession: Accession: Access
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A;Residues: 1-25 <SKI>
A;Ote: this protein displayed charge heterogeneity from variable levels of phosphorylat
C;Superfamily: prolactin
C;Keywords: hormone; phosphoprotein; pitultary
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Pred. No. 1.8e+03;
3; Mismatches 0; Indels
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Best Local Similarity 62.5%; Pred. No. 2.8e+03;
Matches 5; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: PH1634
A; Molecule type: DNA
A; Residues: 1-16 <LEV>
A; Experimental source: bone marrow pre-B lymphocyte C; Keywords: immunoglobulin
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4 DSYYS----PHI 11
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12 NRVOHLHL 19
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=97056061; PubMed=8900406;
Hodnett D.W., Fantozzi D.A., Thurmond D.C., Klautky S.A.,
Hodnett D.W., Estrem S.T., Xu G., Goodridge A.G.;
"The chicken malic enzyme gene: structural organization and
identification of trilodothyronine response elements in the
5'-flanking DNA.";
Arch. Blochem. Blophys. 334:309-324(1996).
--- CATALYTIC ACTIVITY: ($)-malate + NADP(+) = pyruvate + CO(2) +
                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (Fragment).
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-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
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PROSITE; PS00331; MALIC_ENZYMES; PARTIAL
                                  DCMM_PSECH
CT11_LITCI
YMONE_PSEPU
APID_BOMPA
A2M_OCTVU
CT1A_LITCI
CT1B_LITCI
CT3B_LITCI
CXAZ_CONST
APA1_ERYPA
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15 AA; 1842 MW;
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SEQUENCE 15 AA; 1
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Matches 6; Conserv
NCBI_TaxID=9031;
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P85684
P8684
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P81844
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P56587
P22296
P54712
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                               hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                           105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                   1 CGETYYSRVTHPHLPKDIVRSIAKC
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AU33_LITRA
VMO2_CHICK
CXA1_CONCN
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LYC_ESTAC
M117_BOVIN
SODM_HORVU
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CXA4_CONPU
UN05_PINPS
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AU12_LITRA
AU31_LITRA
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YHV4_LACHE
SODM_CANFA
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DMS6_PHYBI
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DCMM_PSECA
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MMPX_SOLTU
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BPP2_BOTIN
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                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 25
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Gaps

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Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
Hydroxylation; Venom; 3D-structure.
         Biochemistry 36:1669-1677(1997).
-!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES,
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND
INHIBIT THEM.
-!- SUBJUSTRY LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
PDB; 1P1P; 07-JUL-97.
                                                                                                                                                                                                  AMIDATION.
9E2147898D697640 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9F4E4678E086C298 CRC64;
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HYDROXYLATION.
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R -> E.
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MEDLINE-99274088; Pubmed-10344291;
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14
15
20
2438 MW;
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11
23
7
13
20
25
2608 MW;
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41.2%;
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Best Local Similarity 41.2
Matches 7; Conservative
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Best Local Similarity 31.2
Matches 5; Conservative
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9 CDKDFY----RPELPR 20
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A-conotoxin PIVA.";
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BPP8_BOTIN
ID BPP8_BOTIN
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VARIANT
NON_TER
SEQUENCE
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MOD_RES
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SEQUENCE
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                                                                                                                                                                      TISSUB-Retrocerebral complex, MEDLINE-99212469; PubMed=10196736; Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.; "Differential distribution of pyrokinin-isoforms in cerebral and abdominal neurohemal organs of the American cockroach."; Insect Biochem. Mol. Biol. 29:139-144(1999).
                                                                                                                                                                                                                                                                        MEDIINE-20189894; Pubmed-10723010;
Predel R., Eckert M.;
"Tagma-specific distribution of FXPRLamides in the nervous system of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hopkins C., Grilley M., Miller C., Shon K.-J., Cruz L.J., Gray W.R., Dykert J., Rivier J., Yoshikami D., Olivera B.M.;
"A new family of Conus peptides targeted to the nicotinic acceptor."
J. Baol. Chem. 270:22361-22367(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                            16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pyrokinin-4 (Pea-PK-4) (YXPRL-amide).
Priplaneta americana (American cockroach).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                            the American cockroach.";
J. Comp. Neurol. 419:352-363(2000)
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY: CORPORA CARDIACA:
-1- TISSUE SPECIFICITY: CORPORA CARDIACA:
-!- MASS SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus purpurascens (Purple cone).
Subtrayoda; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoldea; Conidae; Conus.
NCBI_TaxID=41690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 1; Length 12;
Pred. No. 3.2e+02;
1; Mismatches 1; Indels
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12 AA; 1449 MW; FA7A3049FF42CAA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Alpha-A conotoxin PIVA.
           12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 AA.
                                                                                                                                                              SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                    Neuropeptide; Amidation; Pyrokinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
             PRT;
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MEDLINE-95403432; PubMed-7673220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
             STANDARD;
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                                                                                                                                                                                                                                                              TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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2 HLPHDV 7
           PPK4_PERAM
P82619;
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P55963;
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                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plomion C.; "Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLECTCOPIOLES S 20:1098-1108 (1999).
-I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.6, ITS MW IS: 36 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of needles (N147) (Fragments).
Pinus pinaster (Maritime pine).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ;
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Score 26.5; DB 1; Length 25;
Pred. No. 8.1e+02;
2; Mismatches 7; Indels
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DB 1; Length 15;
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Pred. No. 7.4e+02;
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                Score 25; DB 1;
Pred. No. 8e+02;
                                                                                                                                                                       10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 AA
                                           2; Mismatches
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                17.7%;
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                                           5; Conservative
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                              Best Local Similarity
                                                                      8 RVTHPHLPKDI 18
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2 RFEHENLPQRI 12
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Best Local Similarity
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                                                                                                                                                                                                                                                       enzyme inhibitor)
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8723;
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5 HPQIP 9
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P82386;
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BPP2_BOTIN
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                                           Matches
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"Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";

J. Protein Chem. 9:221-227(1990).

-I. FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADXININ BY INHIBITING THE KINASES THAT INACTIVATE IT.

IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.

PIR; H37196; H37196.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Selbert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
"Characterization of a maleylacetate reductase encoding region from Rhodococcus opecus ICP."
J. Bacteriol. 180:3503-3508(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- Pathway: 3-CHLOROCATECHOL DEGRADATION (BETA-KETOADIPATE PATHWAY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL PRODUCTS AND AS INDUSTRIAL EFFLUENT.

-!- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE
                                                                            Bothrops insularis (Island jararaca) (Queimada jararaca). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eptdosamiria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative maleylacetate reductase II (EC 1.3.1.32) (Fragment).
              ol-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin-potentiating peptide S5,1 (Angiotensin-converting enzyme inhibitor).
                                                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID. 2FF835545761F6D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 1; Le
Pred. No. 5.2e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA.
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PROSITE; PS00913; ADH_IRON_1; PARTIAL.
PROSITE; PS00060; ADH_IRON_2; PARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodococcus opacus (Nocardia opaca)
                                                                                                                                                                                              MEDLINE-90351557; PubMed-2386615;
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          01-APR 1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last seq
01-FEB-1994 (Rel. 28, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                           17.7%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                  10 AA; 1173 MW;
                                                                                                                                                                                                                                                                                                                                       Hypotensive agent; Venom.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.7
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 HPHLP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                  TISSUE-Venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | :: |
S HPNIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAD(P)H
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P56870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-1CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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MCA2_RHOOP
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MEDLINE-90331557; PubMed=2386615;

Cintra A.C.O., Vleira C.A., Giglio J.R.;

Cintra A.C.O., Vleira C.A., Giglio J.R.;

Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";

J. Protein Chem. 9:221-227(1990)

I. Protein Chem. 9:221-227(1990)

I. PROTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF BRADYKININI BY INDIRECT HYPOTENSIVE AGENT.

IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.

PIR; B37196; B37196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Gaps
                                                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin potentiating peptide S4,3,1 (10C) (Angiotensin-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Litoria raniformis (Southern bell frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                          Bothrops insularis (Island jararaca) (Queimada jararaca).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
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MEDLINE-2040845; PubMed=10931191;
ROZEK T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,
Wallace J.C., Tyler M.J.;
"The antibiotic and anticancer active aurein peptides from the
australian bell frogs Litoria aurea and Litoria raniformis the
solution structure of aurein 1.2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 10;
4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRROLIDONE CARBOXYLIC ACID. 30C53546C761F773 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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Litoria raniformis (Southern bell frog), and Litoria urea (Green and golden bell frog).

Eukaryota; Metazoa; Chordan, Craniala; Vertebrata; Euteleostomi; Amphibla; Batrachla; Annra; Neobatrachla; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                          Score 24; DB 1; Length 17;
pred. No. 1.3e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 1; Length 17;
Pred. No. 1.3e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                      F6AC17980428EAFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION.
F6AC0A580428EAFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 AA.
                                                                                                                                                                                                                                    AUREIN 3.1.
AUREIN 3.1.1.
AUREIN 3.1.2.
                                                                                                                                                                                                                                                                          AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: SECRETED. Amidation; Antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                        TISSUE-Granular dorsal gland;
                                                                                                                                                                                                                                                                                                                            17.08;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h
Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 AA; 1769 MW;
                                                                                                                                                                                                                                                                                      17 AA; 1739 MW;
                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                 NCBI_TaxID-116057, 8371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=116057, 8371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND FUNCTION.
                                            SEQUENCE, AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             DIVRSIA 23
                                                                                                                                                                                                                                                                                                                                                                                                     4 DIVKKIA 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU32_LITRA
P82395;
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                                                                                                                                                                                                                                                                         MOD_RES
SEQUENCE
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SEQUENCE
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MEDLINE-20408845; PubMed-10951191;
MEDLINE-20408845; PubMed-10951191;
MEDLINE-20408845; PubMed-10951191;
MROLINE-20408845; PubMed-10951191;
MROLINE-20408845; PubMed-10951191;
MROLINE T. Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,
MADIace J.C., Tyler M.J.;
"The antibiotic and anticancer active aurein peptides from the australian bell frogs Litoria aurea and Litoria raniformis the australian bell frogs Litoria aurea and Litoria raniformis the australian bell frogs Litoria aurea and Litoria raniformis the australian bell frogs Litoria aurea and Litoria raniformis the LINNOCUA, M.LUTEUS, P.WULTOCIDA, S.AUREUS, S.EPIDERMIDIS AND S.UBERIS. PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE. SHOWS ANTICANCER ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                            Gaps
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2003 (Rel. 41, Last annotation update)
Aurein 3.1 (Contains: Aurein 3.1.1; Aurein 3.1.2).
Litoria raniformis (Southern bell frog), and Litoria aurea (Green and golden bell frog).
Eukaryota; Metazoa; Chordeta; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylldae;
                                                                                                                                                                                                                                                                                                                                                 Litoria raniformis (Southern bell frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
EUI. J. BLOCHEM. 267:5330-5341(2000).
-1- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
L.INDOCHA MND S.UBERIS. PROBABLY ACTS BY DISTURBING MEMBRANE
FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.
-1- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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Pred. No. 9.7e+02;
3; Mismatches 1; Indels
                                                                                                                                 Score 24; DB 1; Length 13; Pred. No. 9.7e+02;
                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION.
1EACB99DFBC83330 CRC64;
                                                                                AMIDATION.
173CB99DFBC83330 CRC64;
                                                                                                                                                                                                                                                                                                 01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                         13 AA
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                                                                                                                                                         3; Mismatches
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                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                 17.0%;
50.0%;
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50.0%;
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SEQUENCE 13 AA; 1447 MW;
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                                                                                                                                                          4; Conservative
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                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=116057;
                                                                                                                                                                                                 ||:: ||:
4 DIIKKIAE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 DIVRSIAK 24
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4 DIIKKIAE 11
                                                                                                                                                                                  17 DIVRSIAK 24
                                                                                                                                                                                                                                                                         AU12_LITRA
P82387;
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P82394;
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                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                          Litoria
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AU12_LITRA
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3D-structure
 20
20 AA;
                                                        Best Local Similarity
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P56973;
 NON_TER
SEQUENCE
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MOD_RES
SEQUENCE
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CXA1_CONCN
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                                                                     Matches
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McDLINE-20408845; PubMed=10951191;

Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,

Wallace J.C., Tyler M.J.;

"The antiblotic and anticancer active aurein peptides from the
australian bell frogs Litoria aurea and Litoria raniformis the
solution structure of aurein 1.2.;

Eur. J. Blochem. 267:5330-5341(2000).

-- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST L.LACTIS, M.LUTEUS,

PP. MULTOCIDA, S.AURRUS, S.EPIDERMIDIS AND S.UBERIS. PROBABLY ACTS

BY DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Vitelline membrane outer layer protein II (VMO-II) (VMOII) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane.";
Biochem. J. 286:17-22(1992).
-!- FUNCTION: EXACT FUNCTION NOT KNOWN, COMPONENT OF THE OUTER
MEMBRANE OF THE VITELLINE LAYER OF THE EGG.
-!- PTM: ALL CYSTEINE RESIDUES OF THE MATURE PROTEIN ARE INVOLVED IN
DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kido S., Morimoto A., Kim F., Doi Y.; ^{\circ} Isolation of a novel protein from the outer layer of the vitelline
                                                                                      01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Aurein 3.3 [Contains: Aurein 3.3.1]
Litoria raniformis (Southern bell frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                             Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.0%; Score 24; DB 1; Length 17; 71.4%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                 AUREIN 3.3.
AUREIN 3.3.1.
AMIDATION.
F6ACOA471428EAFD CRC64;
                                                                   17 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                 SHOWS ANTICANCER ACTIVITY.
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Egg yolk;
MEDLINE=92392273; PubMed=1520265;
                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES 17 17
SEQUENCE 17 AA; 1797 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 71.4
Matches 5; Conservative
                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                          SEQUENCE, AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                        Amidation; Antibiotic
                                                                                                                                                                                  NCBI_TaxID=116057;
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| | | | : | | 4 DIVKKIA 10
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Q9PS49;
                                                                   AU33_LITRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                          Litoria.
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                                            RESULT 12
AU33_LITRA
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VMO2_CHICK
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MEDLINE-99255390; PubMed-10320362;
MEDLINE-99255390; PubMed-10320362;
Favreau P., Krimm I., le Gall F., Bobenrieth M.J., Lamthanh H.,
Bouet F., Servent D., Molgo J., Menez A., Letourneux Y.,
Lancelin J.-M.;
"Biochemical characterization and nuclear magnetic resonance
structure of novel alpha-conotoxins isolated from the venom of Conus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELOWGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
PDB3: 1845; 09-JUL-99.
Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 38:6317-6326(1999).

-!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS INHIBIT THEM. THIS PEPTIDE SEEMS TO BE A POTENT AND SELECTIVE BLOCKER OF MUSCULAR SUBTYPE OF NACHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23.5; DB 1; Length 14; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-conotoxin CnIA [Contains: Alpha-conotoxin CnIB].
Conus consors (Singed cone).
Eukaryota: Metazoa: Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conus magus (Magus cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                             Score 24; DB 1; Length 20, Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
20
2325 MW; 45FC7989AB7527C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION.
DEEE91969BF5E5BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA-CONOTOXIN CNIA. ALPHA-CONOTOXIN CNIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
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                                                                                                                                                                                                                                                                                                                                                                                                         14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.78;
71.48;
                                                                                                      17.0%;
44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 14
14 14
14 AA; 1548 MW;
                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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NCBI_TaxID=6492;

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-1- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
PIR: A01784; NTKNIM.
POSTSYNAPLIC neurotoxin; Acetylcholine receptor inhibitor; Amidation; Venom.
                         SEQUENCE.
MEDLINE-83073458; PubMed-7149738;
McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;
"Isolation and structure of a peptide toxin from the marine snail
Conus magus.";
Arch. Biochem. Biophys. 218:329-334(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                      MEDLINE-89024586; Pubmed-3052286;
Gray W.R., Olivera B.M., Cruz L.J.;
"Peptide toxins from venomous Conus snails.";
Annu. Rev. Blochem. 57:665-700(1988).
-!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
INHIBIT THEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                  DISULPIDE BONDS.

MEDILINE—8000DS.

Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;

"Conotoxin MI. Disulfide bonding and conformational states.";

J. Biol. Chem. 258:12247-12251(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.3%; Score 23; DB 1; Length 14; 60.0%; Pred. No. 1.5e+03; Artive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       3 8
4 14
14 14 AMIDATION.
14 AA; 1499 MW; DEEE91898BF5E5BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 60.0 Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGETY 5
                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
MOD_RES
SEQUENCE
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Search completed: August 26, 2002, 10:30:17 Job time: 637 sec

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